

FIG. 1A

BHR (PC20 \leq 16 mg/ml) & Asthma

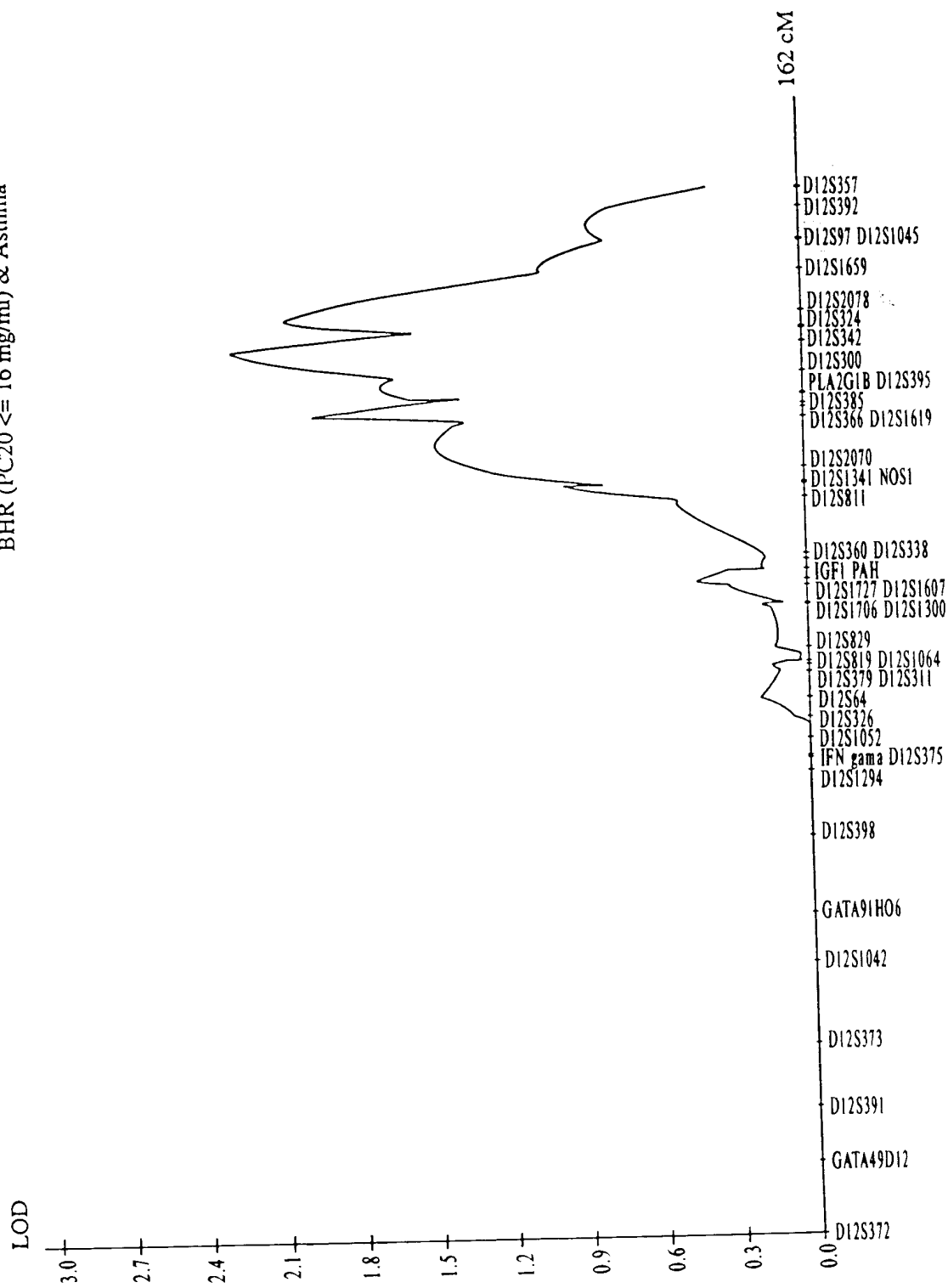


FIG. 1B

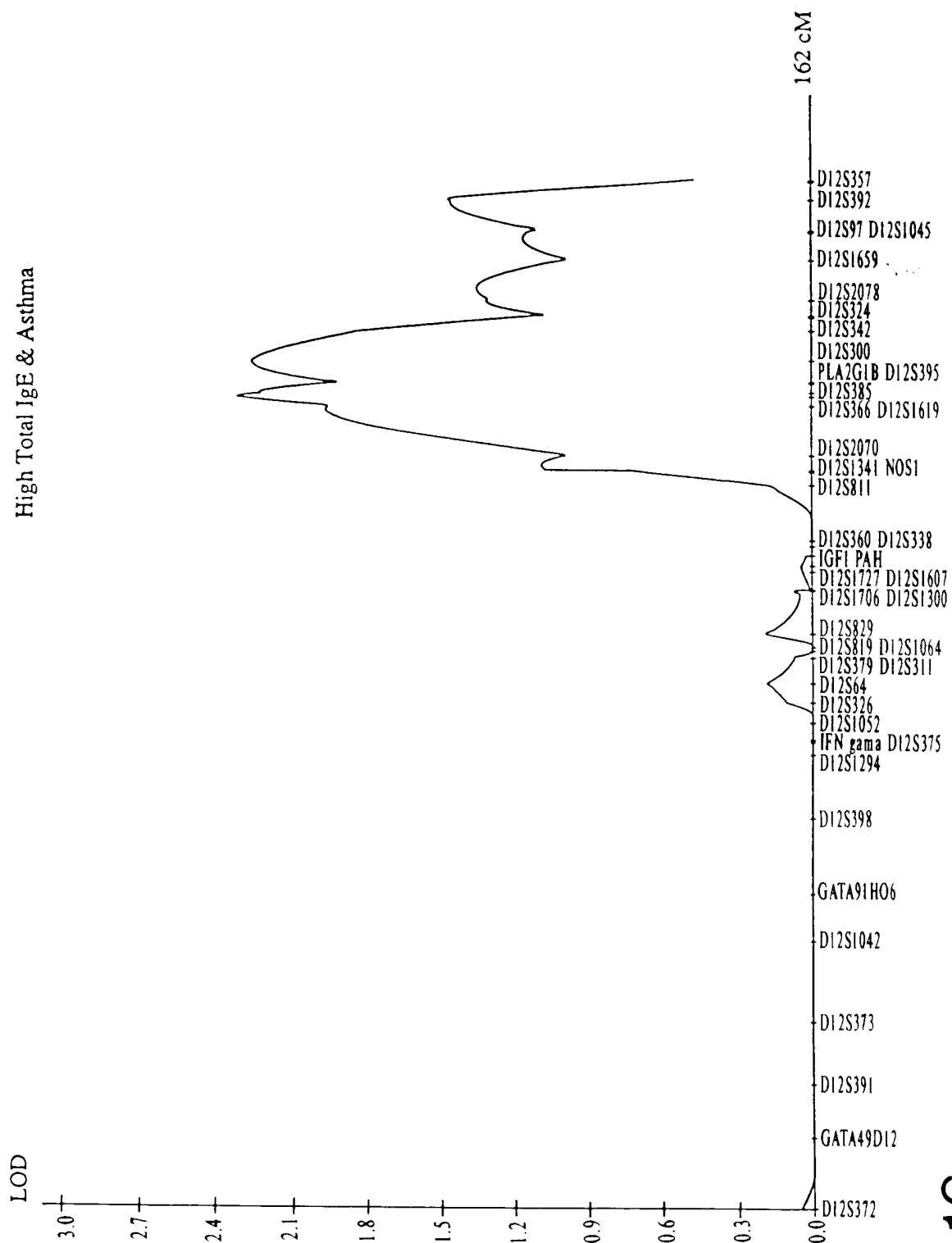


FIG. 1C

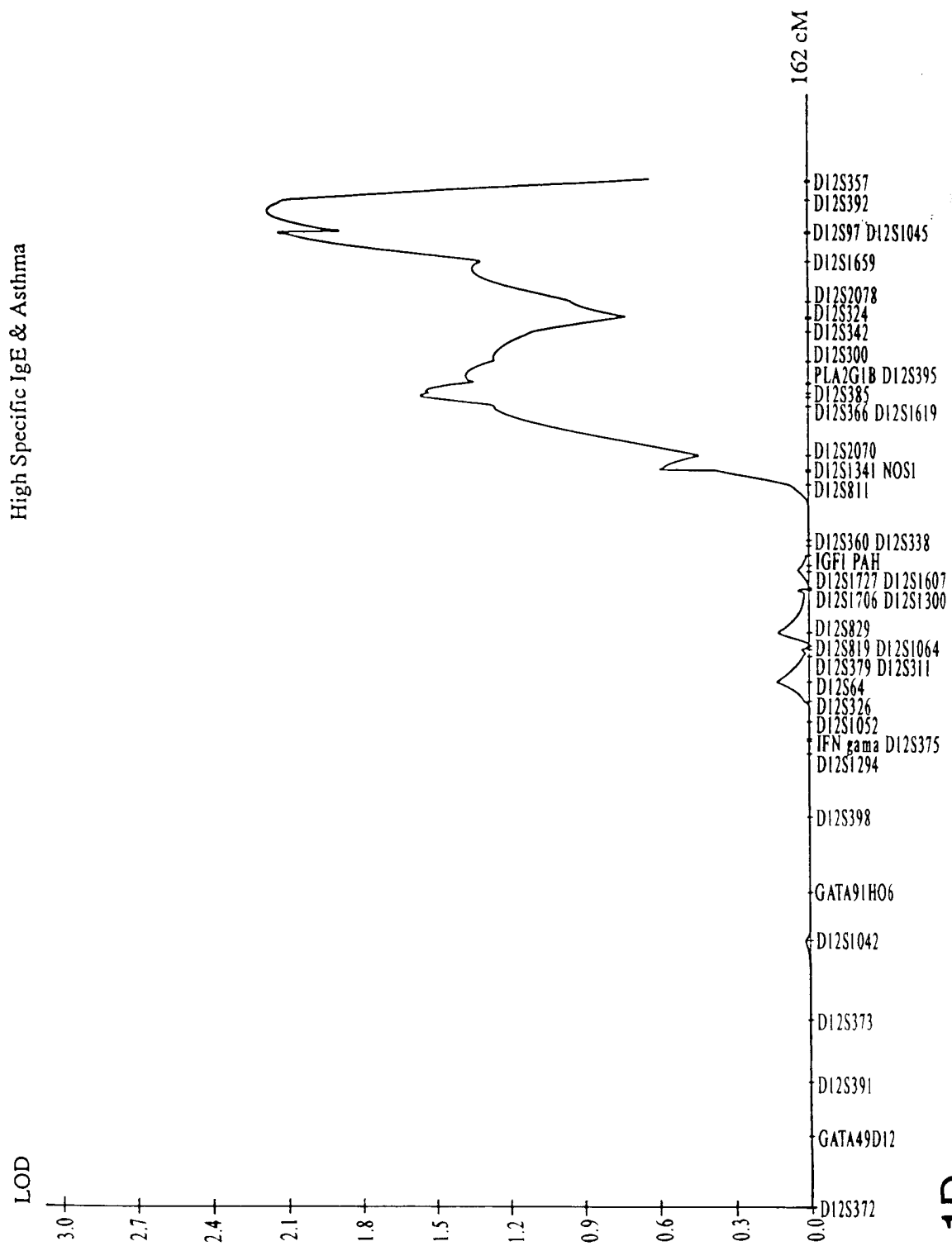
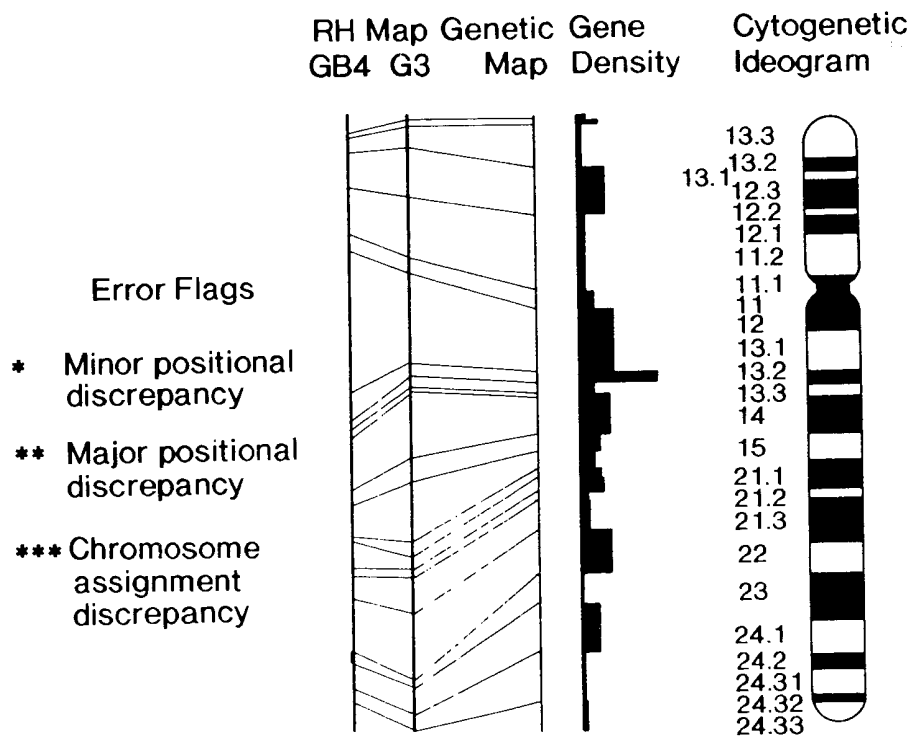


FIG. 1D

Chromosome 12: D12S79-D12S366



The interval shown is on the GB4 map
 See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S79 (126.1 cM)
Bottom of interval:	D12S366 (133.8 cM)
Genetic size of bin:	8 cM
Physical size of bin:	9 cR3000

FIG. 2A

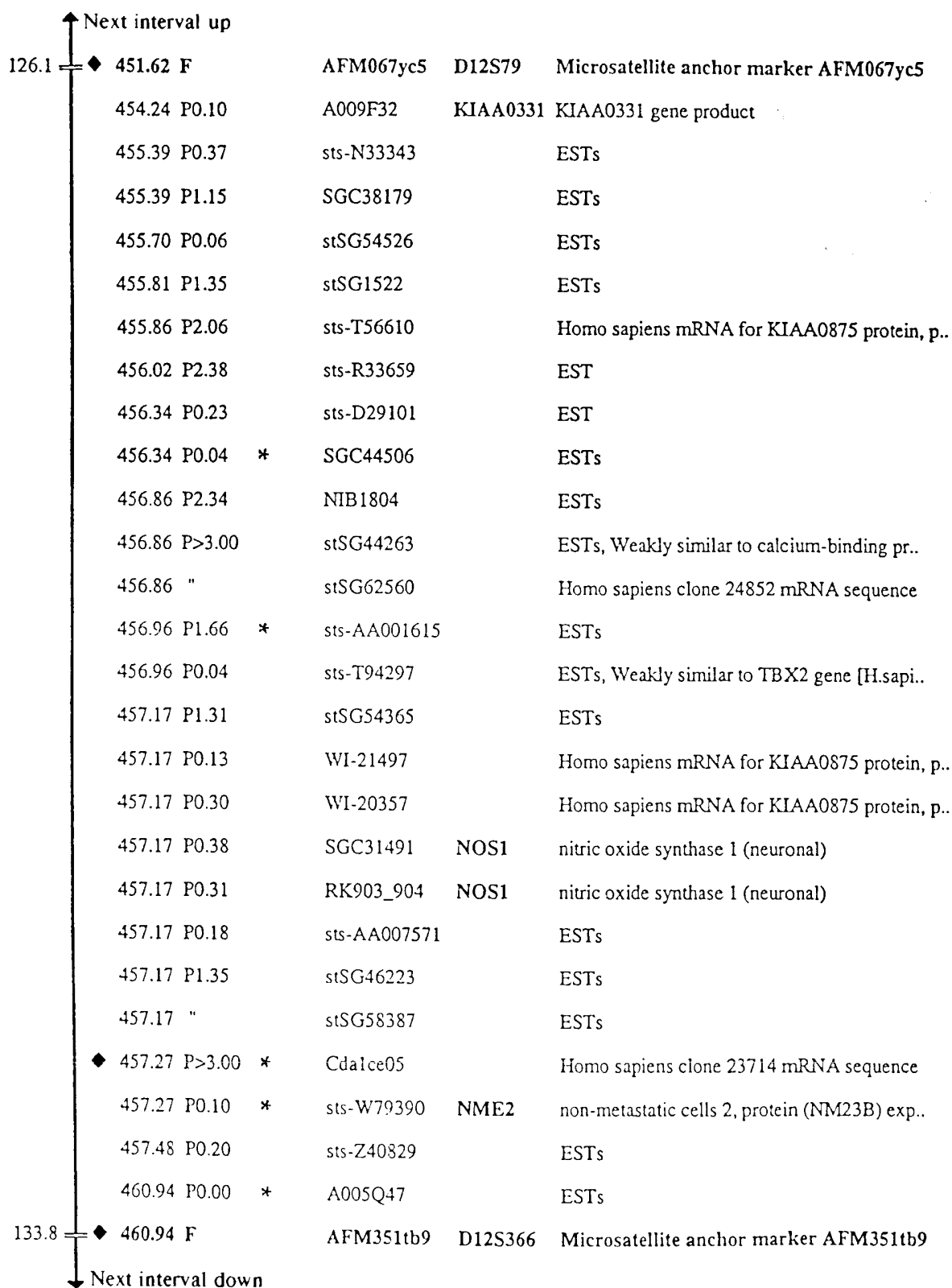
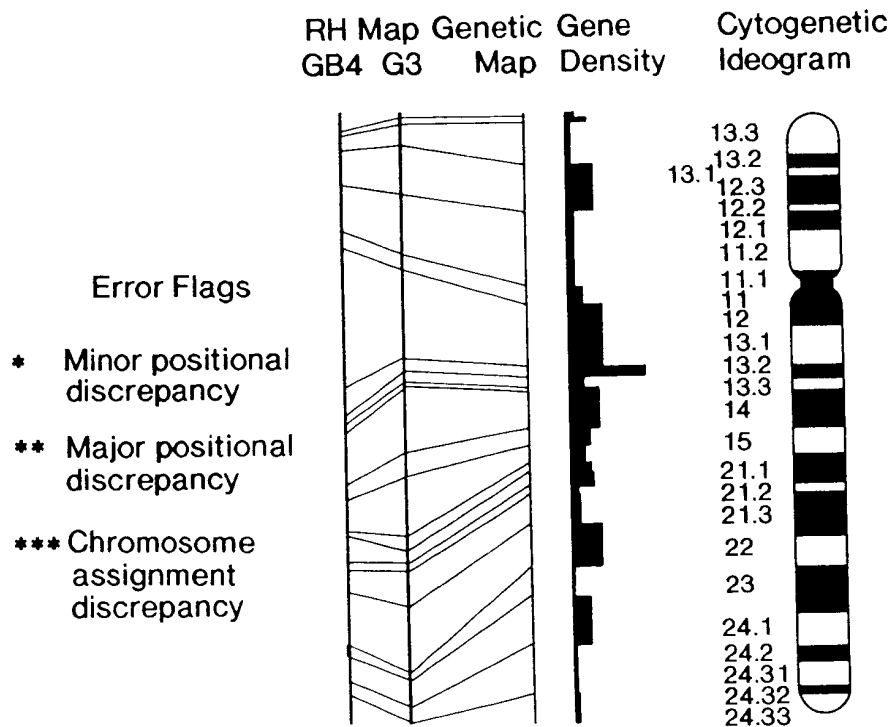


FIG. 2B

Chromosome 12: D12S366-D12S340



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S366 (133.8 cM)
Bottom of interval:	D12S340 (147.5 cM)
Genetic size of bin:	14 cM
Physical size of bin:	21 cR3000

133.8	↑ Next interval up	◆ 460.94 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
		462.85 P1.00 *	stSG8109		ESTs
		462.85 "	sts-X75252	PBP	prostatic binding protein
		462.95 P1.04	sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2C

463.77	P0.19	WI-16745		Human clone 37, 5cM region surrounding hepa..
◆ 463.77	P0.20	SGC33949	KIAA0262	KIAA0262 gene product
463.98	P0.02	A008B04		ESTs
463.98	"	stSG50309		ESTs
463.98	"	stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
463.98	P0.04	stSG27318		Human clone 23932 mRNA sequence
463.98	P0.08	R06295		EST
463.98	P1.33	sts-W56792		ESTs
464.08	P2.32	A007E48		ESTs
464.19	P1.28	A009U43		ESTs
464.29	P1.33	stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
464.39	P1.09	sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
464.39	P1.13	stSG15685	KIAA0262	KIAA0262 gene product
464.39	"	RP_P0_1	RPLP0	Ribosomal protein large, P0
464.39	P1.09	stSG29626		ESTs
464.39	P1.14	stSG31407		Human DNA sequence from BAC 15E1 on chrom..
464.39	"	A001T32	PXN	paxillin
464.39	"	A001W18		H.sapiens mRNA for AMP-activated protein ..
464.39	"	WIAF-40		Human mRNA for KIAA0219 gene, partial cds
464.39	"	sts-T95105		ESTs
464.39	"	Cda0id01		ESTs
464.39	P1.13	stSG31431		ESTs, Moderately similar to (define not a..
◆ 464.39	"	* WI-13177		Homo sapiens clone 23714 mRNA sequence
464.39	"	IB1092		Homo sapiens clone 23714 mRNA sequence
464.39	"	T79466		ESTs
464.39	P1.18	stSG48379		ESTs
464.45	P1.05	KIAA0219		Human mRNA for KIAA0219 gene, partial cds
464.45	"	stSG40392		ESTs
464.45	"	stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆ 464.49	P0.21	A006F12	KIAA0152	KIAA0152 gene product
464.49	P0.25	sts-AA002185	PXN	paxillin
464.49	P0.10	stSG48442		ESTs
464.49	"	sts-T16456		ESTs
464.49	"	stSG62260		ESTs

FIG. 2D

	464.49	"	NIB1331		ESTs
	464.49	"	WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49	"	WIAF-1058		ESTs, Moderately similar to unknown [H.sap..
	464.49	"	SGC34758		ESTs
	464.49	"	WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
	464.49	"	IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49	"	SGC32343		ESTs
	464.79	P0.96	SGC33521		ESTs
	464.79	P0.96	* X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
	465.20	P0.20	sts-H10302		ESTs
◆	465.38	P0.85	A007E11	KIAA0262	KIAA0262 gene product
	465.41	P0.81	A007I44	RPLP0	ribosomal protein, large, P0
	465.41	"	stSG22726		EST
	465.41	"	WI-17776		ESTs
	465.41	"	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41	"	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41	P0.77	stSG4775	SFRS9	splicing factor, arginine/serine-rich 9
	465.41	"	A002J47		ESTs, Weakly similar to heat shock protein..
	465.41	P0.80	stSG46660		EST
	465.51	P0.75	stSG41086	PXN	paxillin
	465.51	P0.83	stSG52121		ESTs
	465.91	P0.01	WI-16071		ESTs
	465.91	P0.00	WI-13962		H.sapiens mRNA for AMP-activated protein ..
	466.62	P0.00	sts-AA011220	SFRS9	splicing factor, arginine/serine-rich 9
	466.71	P0.00	stSG4712		ESTs, Weakly similar to homology with o251..
	466.91	P0.01	WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
	466.91	P0.01	D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
	467.01	P0.01	stSG52567		ESTs
135.1	467.11	F	AFM123xh2	D12S86	Microsatellite marker AFM123xh2
135.1	467.11	P0.01	AFM299zd5	D12S349	Microsatellite marker AFM299zd5
	467.11	P0.01	AFM123xh2		Unknown
137.5	◆ 467.21	P0.02	AFM220zf4	D12S321	Microsatellite marker AFM220zf4
	467.21	P0.02	sts-W73277	SFRS9	splicing factor, arginine/serine-rich 9
	467.21	P0.02	stSG8721		EST

FIG. 2E

467.21 "	stSG44224		ESTs
467.21 "	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆ 467.21 "	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
467.21 "	stSG47820		ESTs
467.21 "	Bdac4h06	KIAA0262	KIAA0262 gene product
467.21 "	stSG15021		ESTs
467.21 "	A002B13	SFRS9	splicing factor, arginine/serine-rich 9
◆ 467.21 "	H50549	KIAA0262	KIAA0262 gene product
467.21 P0.03	SGC35167		EST
467.21 P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
467.21 P0.02	WIAF-607		Unknown
467.31 P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
468.93 P0.85	SGC31344		EST
469.13 P0.90	A007C39	A CAD5	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
469.13 P0.14	stSG35104		ESTs
469.13 "	A006Q41		Unknown
469.23 P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
469.33 P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sap..
469.33 "	R01708		EST
469.33 "	stSG54819	HICALB_BR	calbrain
469.33 "	A001Z45		ESTs, Highly similar to (define not avail..
469.33 "	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..
469.33 "	stSG63173		EST
469.33 "	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
469.42 P1.01	WI-16068		EST
469.44 P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62627		EST
469.44 "	stSG36007		Homo sapiens full length insert cDNA clone..
469.44 "	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
469.44 "	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62591		ESTs
◆ 469.54 P1.03	A006N38	KIAA0152	KIAA0152 gene product
469.62 P1.03	sts-N34573		ESTs
469.62 P1.03	sts-N58045		ESTs

FIG. 2F

469.62	P1.04		WI-13224		EST
469.83	P1.12		SGC34424		ESTs
469.93	P1.14		stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.14	P1.17		stSG52516		ESTs, Weakly similar to (define not avail..
470.24	P1.32		D0S1735E		ESTs
470.24	P1.12		WI-6178		ESTs
470.32	P1.25		sts-U29895		Unknown
470.32	P1.24		WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.43	P1.29		stSG52094		ESTs
470.63	P1.38		A004O17		ESTs
◆ 470.77	P1.32	**	SGC33451		ESTs, Weakly similar to rhoHP1 [H.sapiens..
◆ 470.84	P1.35	**	sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..
470.84	P1.52		WI-13062		Homo sapiens mRNA, expressed in fibroblast..
471.27	P1.60		sts-R99269		EST
471.37	P1.70		stSG1991		ESTs
471.37	"		stSG15859		Homo sapiens full length insert cDNA YQ02..
471.58	P1.78		stSG29729		ESTs, Weakly similar to (define not avail..
471.58	P1.37		WI-16979		ESTs
471.65	P1.39		WI-17693		EST
471.80	P1.29		WI-22060		ESTs
471.90	P>3.00		stSG8210		ESTs, Moderately similar to neuronal threa..
471.90	"		WI-17956		EST
471.90	"		WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
471.90	"		stSG47029		ESTs
471.90	"		stSG47647		EST
471.90	"		sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆ 471.90	"	**	WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..
471.90	"		NIB962		ESTs
471.90	"		A009E34		ESTs, Moderately similar to neuronal threa..
471.90	"		sts-T17477		ESTs
472.08	P1.49		sts-X89984		H.sapiens mRNA for BCL7A protein
472.12	P>3.00		SGC34693		EST
472.12	P>3.00		A009O01		ESTs, Weakly similar to neuronal thread pr..
472.29	P>3.00		stSG47084		ESTs

FIG. 2G

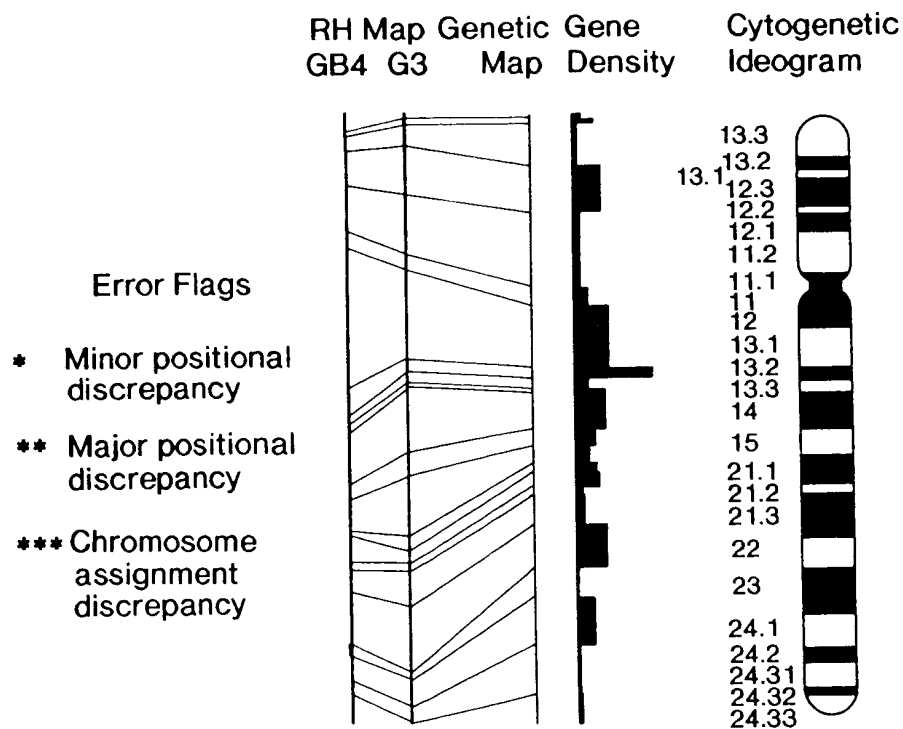
472.40 P>3.00	stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
472.40 P>3.00	AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
472.61 P>3.00	A002R44		Unknown
472.61 P>3.00	SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
472.72 P0.01	sts-H98108		ESTs
472.97 P>3.00	WI-6239		ESTs
473.04 P>3.00	sts-H75490		ESTs
◆ 473.58 P>3.00 **	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
474.01 P>3.00	stSG8610		ESTs
474.01 P>3.00	stSG47080		ESTs
474.38 P2.18	stSG8686		ESTs, Weakly similar to similar to pre-mRN..
474.38 P2.25	stSG26358		ESTs, Weakly similar to similar to pre-mRN..
474.38 "	stSG29931		ESTs
474.38 "	WI-17926		ESTs
474.38 "	WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
474.38 "	1834		EST
474.38 P2.26	sts-X98258	MPP-9	M phase phosphoprotein 9
474.38 P2.39	stSG40753		ESTs
474.64 P>3.00	A004D47		ESTs, Highly similar to There are three pu..
474.64 P>3.00	sts-N23129	MPP-9	M phase phosphoprotein 9
474.75 P2.41	sts-AA040696		ESTs
474.81 P2.37	sts-AA022496		ESTs
474.81 P2.28	stSG46930	MPP-9	M phase phosphoprotein 9
474.97 P>3.00	WI-20552	DRP	density-regulated protein
475.02 P>3.00	SGC30324		ESTs
475.07 P>3.00	D10923	HM74	putative chemokine receptor; GTP-binding pr..
475.07 P>3.00	stSG2418	DOC1	Deleted in oral cancer-1
475.07 "	stSG21321		ESTs
475.07 "	stSG53515	MPP-9	M phase phosphoprotein 9
475.07 P>3.00	SGC31687	DOC1	Deleted in oral cancer-1
475.07 P>3.00	WIAF-214	HM74	putative chemokine receptor; GTP-binding pr..
475.13 P0.79	sts-W93806		ESTs
475.13 P2.13	stSG48145		ESTs
475.18 P2.34	A003B12		Homo sapiens full length insert cDNA clone..

FIG. 2H

	475.18 P>3.00	WI-22211		Homo sapiens full length insert cDNA clone..
	475.18 P2.08	stSG48093		ESTs
	475.18 "	A004P27		ESTs, Weakly similar to MULTIDRUG RESI..
	475.35 P2.10	stSG9904		ESTs
	475.40 P0.45	sts-AA024696		ESTs
	475.51 P>3.00	stSG53793		ESTs
	476.10 P>3.00	Bda98d05		Homo sapiens full length insert cDNA clone..
	476.21 P>3.00	sts-H24468		ESTs
	476.21 P>3.00	sts-N94741		ESTs
	476.64 P0.28	stSG22488		ESTs
	476.85 P0.36	stSG44909		ESTs
	477.06 P0.10	stSG54797		ESTs
	477.27 P1.33	stSG48099		ESTs
	477.37 P0.09 *	sts-AA028894		Homo sapiens silencing mediator of retinoic..
	477.80 P1.44	stSG52727		EST
	477.80 "	U44799		Human U1-snRNP binding protein homolog mR..
	477.80 "	WI-15963		ESTs
	477.80 "	stSG53886		ESTs, Weakly similar to neuronal thread pr..
	478.74 P0.01	WIAF-364		ESTs
	479.01 P0.21	WI-21080		ESTs
	479.13 P0.19	A009B29		ESTs
	479.33 P0.22	A006F32	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19	WIAF-449	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19 *	WI-15890		H.sapiens mRNA for transmembrane protein r..
	479.55 P0.20 *	stSG349		H.sapiens mRNA for transmembrane protein r..
	479.55 " *	A004O46	BDKRB2	bradykinin receptor B2
	479.55 "	stSG42540		ESTs
	479.55 "	sts-N26791		ESTs
	479.55 "	stSG53943		ESTs
	479.55 "	stSG49468		EST
145.7	479.74 P0.16	AFM294ze9	D12S342	Microsatellite marker AFM294ze9
	481.46 P0.00	sts-AA007694		EST
147.5	◆ 481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
	Next interval down			

FIG. 2I

Chromosome 12: D12S340-D12S97



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S340 (147.5 cM)
Bottom of interval:	D12S97 (160.9 cM)
Genetic size of bin:	13 cM
Physical size of bin:	13 cR3000

<div> <div>↑ Next interval up</div> <div>147.5</div> </div>				
◆	481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
	481.66 P0.00	SGC31838		ESTs
	483.18 P0.70	stSG48255		ESTs
	483.58 P0.69	stSG47315		ESTs

FIG. 2J

483.87	P0.83	stSG47707	ESTs
484.70	P0.93	stSG4060	ESTs
484.70	"	stSG62390	GTF2H3 general transcription factor IIIH, polypepti..
484.70	"	stSG42994	ESTs
484.73	P0.74	stSG46906	ESTs
484.80	P0.91	A004X33	ESTs
484.91	P1.11	stSG3211	ESTs, Weakly similar to B-cell growth fact..
484.91	" *	sts-Z41302	BDKRB2 bradykinin receptor B2
484.91	" *	sts-Z41302	BDKRB2 bradykinin receptor B2
484.91	"	sts-T58259	ESTs, Weakly similar to B-cell growth fact..
484.91	"	stSG52737	ESTs
484.91	"	Bda03b10	UBC ubiquitin C
484.91	"	stSG1936	CD36L1 CD36 antigen (collagen type I receptor, thr..
484.91	"	sts-AA017225	ESTs
484.91	P1.15	WI-12212	ESTs
485.12	P1.18	A004F14	ESTs
485.12	P1.18	SGC31333	ESTs
485.23	P1.21 *	WI-12482	BDKRB2 bradykinin receptor B2
485.23	P1.07	sts-AA017698	ESTs
485.33	P1.22	WI-12422	ESTs
485.51	P1.18	stSG42398	EST
485.64	P1.04	sts-AA009669	ESTs
486.07	P2.50	stSG21539	EST
486.13	P1.44	WI-12439	EST
486.34	P1.26	sts-W31616	UBC ubiquitin C
486.38	P>3.00	stSG54715	ESTs
486.76	P1.64 *	WI-6921	H.sapiens mRNA for transmembrane protein r..
487.08	P>3.00	WI-13120	Human mRNA for KIAA0318 gene, partial cds
487.23	P>3.00	stSG54353	ESTs
487.23	P>3.00	stSG22703	EST
487.28	P>3.00	stSG62698	ESTs
487.28	P>3.00 *	sts-D60472	Homo sapiens silencing mediator of retinoic..
487.28	P>3.00	stSG36097	ESTs
487.33	P1.36	sts-U37146	Homo sapiens silencing mediator of retinoic..

FIG. 2K

	487.50 P>3.00	stSG9807	ESTs
	487.50 P>3.00	stSG15434	ESTs
	487.60 P>3.00	stSG53251	ESTs
	487.60 P>3.00	stSG30525	SRRP129 SC35-interacting protein 1
	487.60 P>3.00	stSG46424	ESTs
	487.70 P>3.00	A007A34	ESTs
154.4	487.75 P2.00	AFMa197zd9	D12S1609 Microsatellite marker AFMa197zd9
	487.75 P2.02	A006D44	ESTs
	487.80 P>3.00	SGC30248	ESTs, Weakly similar to peptide/histidine ..
	488.07 P1.68	stSG6320	Homo sapiens clone 24617 mRNA sequence
	488.07 P1.66	stSG6305	Homo sapiens clone 24790 mRNA sequence
	488.07 P0.02	sts-N20163	Homo sapiens full length insert cDNA clone..
	488.12 P>3.00	stSG60065	ESTs
	488.12 P>3.00	stSG47723	ESTs
	488.44 P1.59	stSG3292	Homo sapiens clone 24790 mRNA sequence
	488.44 P0.03	WIAF-856	EST, Weakly similar to reverse transcripta..
	488.65 P1.54	WI-12272	Homo sapiens clone 24790 mRNA sequence
	488.65 P1.82	stSG52343	ESTs
	488.82 P1.80	stSG16387	CPN2 carboxypeptidase N, polypeptide 2, 83kD
	488.97 P1.80	SGC31722	ESTs
	489.07 P0.06	stSG54325	ESTs
	489.07 P>3.00	stSG63473	ESTs
160.9	◆ 489.07 P>3.00	AFMa123xel	D12S367 Microsatellite marker AFMa123xel
	489.14 P0.17	sts-T81113	ESTs
	489.29 P0.05	sts-AA025438	EST
	489.50 P1.37 ***	Cdalad08	ESTs
	489.50 P0.05	WI-15018	ESTs
	489.50 P1.50	WI-18492	ESTs
	489.57 P1.48	WI-16177	Homo sapiens androgen receptor associated p..
	489.67 P1.44	stSG53307	ESTs
	489.71 P1.43	stSG53541	Homo sapiens hiwi mRNA, partial cds
	489.71 P1.43	stSG9546	Homo sapiens clone 24617 mRNA sequence
	489.89 P1.56	A006O16	ESTs
	490.10 P1.42	H64839	EST

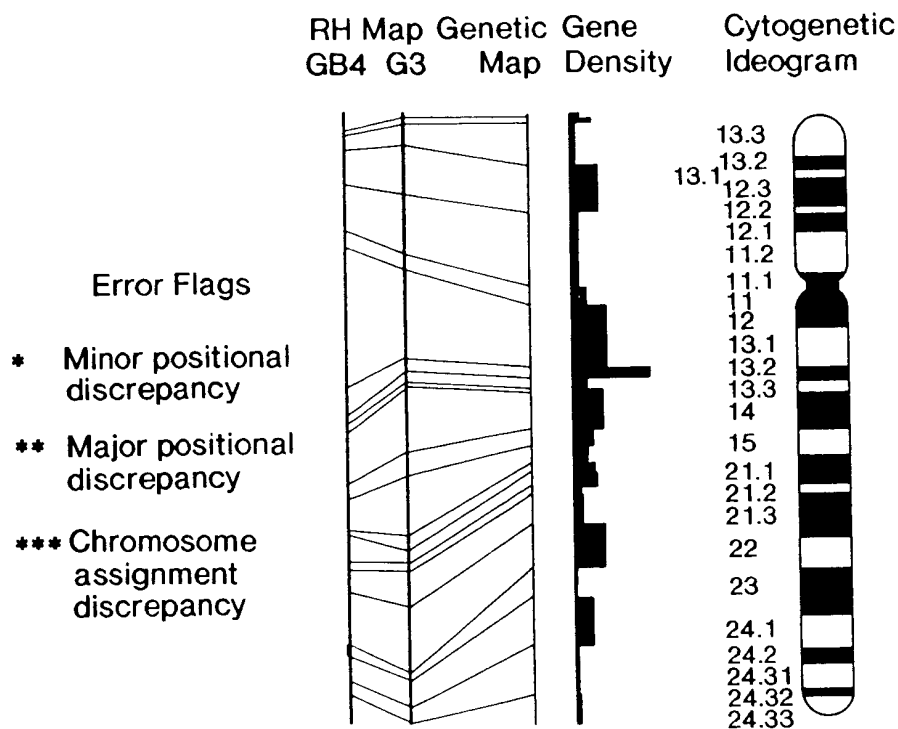
FIG. 2L

160.9 —◆ 490.20 P0.05
494.19 F
↓ Next interval down

stSG43910 SFRS8 splicing factor, arginine/serine-rich 8 (sup..
AFM210zd6 D12S97 Microsatellite anchor marker AFM210zd6

FIG. 2M

Chromosome 12: D12S97-qTEL



About This Interval

Top of interval:	D12S97 (160.9 cM)
Bottom of interval:	chr12_qTEL (169.1 cM)
Genetic size of bin:	8 cM
Physical size of bin:	172 cR3000

	Next interval up			
160.9	◆ 494.19 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6
	498.06 P0.02	stSG53600		ESTs, Weakly similar to peptide/histidine ..
	499.71 P1.73	stSG3357		ESTs
165.7	499.71 "	AFM295ye9	D12S343	Microsatellite marker AFM295ye9

FIG. 2N

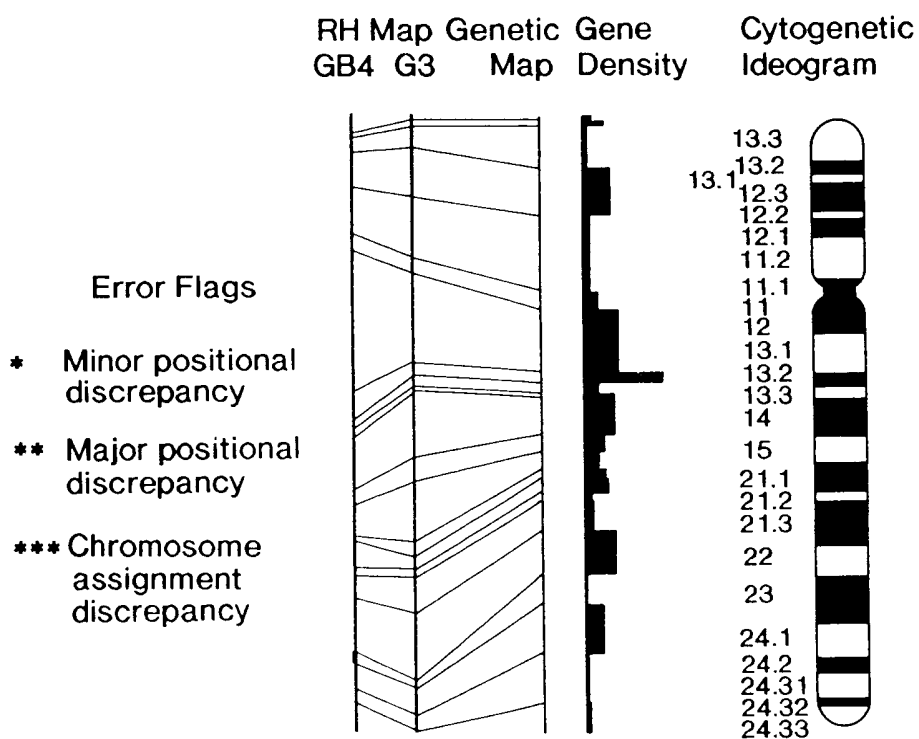
499.71 P1.72	stSG30906	ESTs
499.71 "	stSG43796	MMP17 matrix metalloproteinase 17 (membrane-insert..
499.71 P1.71	sts-X89576	MMP17 matrix metalloproteinase 17 (membrane-insert..
499.92 P>3.00	stSG43769	ESTs
500.50 P1.88	stSG26056	ESTs
500.50 P2.33	SGC30786	KIAA0331 KIAA0331 gene product
500.61 P>3.00	stSG1702	Homo sapiens CAGH32 mRNA, partial cds
500.61 "	sts-N59820	ESTs
500.61 "	stSG42115	KIAA0331 KIAA0331 gene product
500.61 "	IB2452	ULK1 unc-51 (C. elegans)-like kinase 1
500.61 "	stSG52521	ESTs
500.61 "	FB9F8	ESTs, Weakly similar to PUTATIVE ATP-D..
500.61 "	AA252357	ESTs
500.61 "	stSG4720	Homo sapiens pseudouridine synthase 1 (PUS..
500.61 "	sts-AA001424	KIAA0331 KIAA0331 gene product
500.61 P>3.00	stSG31443	ESTs
500.61 P>3.00	stSG49622	ULK1 unc-51 (C. elegans)-like kinase 1
500.61 P2.49	stSG50559	ESTs
501.04 P1.10	stSG54842	ESTs
501.04 P2.03	A008Y05	Unknown
501.89 P2.18	stSG39493	Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	A002A44	Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	sts-H94865	EST
501.99 P>3.00	R50113	ESTs
502.10 P1.75	stSG48386	ESTs
502.10 "	stSG50504	ESTs
502.63 P0.06	A006R19	ESTs
502.63 P1.06	WIAF-864	ESTs
502.94 P1.51	stSG54813	ESTs, Weakly similar to peroxisome membran..
503.04 P1.42	A004B47	ESTs, Highly similar to DNA polymerase ep..
503.25 P0.28	stSG27206	ESTs
503.25 "	stSG40199	Homo sapiens mRNA for KIAA0692 protein, p..
503.46 P0.23	stSG8935	ESTs
504.68 P0.69	stSG4731	Homo sapiens mRNA for KIAA0692 protein, p..

FIG. 20

169.1	504.68 "	A005Q05		ESTs
	504.68 "	stSG8142		ESTs, Highly similar to DNA polymerase ep..
	506.39 F	AFM310vd5	D12S357	Microsatellite marker AFM310vd5
	506.39 P0.02	A005X42		Homo sapiens mRNA for KIAA0692 protein, p..
	508.59 P0.78	Cda18g06		ESTs
	◆ 508.59 P0.78 **	Cda1jf08		Homo sapiens mRNA for GCP170, complete cd..
	508.59 P0.54	R39599		ESTs
	509.98 P0.10	stSG31494	ZNF140	zinc finger protein 140 (clone pHZ-39)
	509.98 P0.16	stSG40222		ESTs
	509.98 "	sts-R55615		ESTs, Weakly similar to zinc finger protei..
	509.98 "	sts-R02295		ESTs
	509.98 "	sts-R81342		ESTs
	511.20 F	TEL-12q82		Marker TEL-12q82
	512.81 P0.20	sts-H65839		ESTs, Weakly similar to transformation-rel..
	514.97 P0.36	stSG46141		ESTs, Weakly similar to zinc finger protei..
	514.97 P0.90	stSG52998		ESTs
	519.10 P1.77	A008W21	CYP51	cytochrome P450, 51 (lanosterol 14-alpha-de..
	519.54 P0.81	stSG52716		ESTs
	● TELOMERE			

FIG. 2P

Chromosome 12: D12S79-D12S366



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

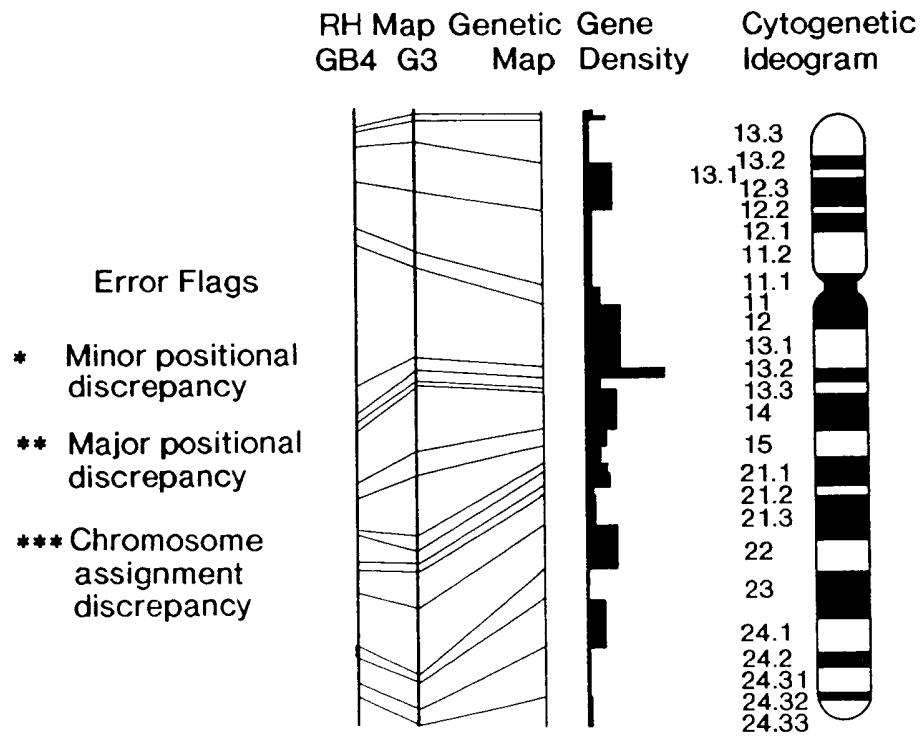
Top of interval:	D12S79 (126.1 cM)
Bottom of interval:	D12S366 (133.8 cM)
Genetic size of bin:	8 cM
Physical size of bin:	63 cR ₁₀₀₀₀

FIG. 3A

					Next interval up
126.1	◆ 4955 F	AFM067yc5	D12S79	Microsatellite anchor marker AFM067yc5 (SHGC-692)	
129.2	4988 F	AFMa067we1	D12S1718	Microsatellite marker AFDa067we1 (SHGC-20..	
	◆ 5007 F *	SHGC-2657		Homo sapiens clone 23714 mRNA sequence	
	◆ 5014 F *	SHGC-2653		Homo sapiens clone 23714 mRNA sequence	
133.8	◆ 5018 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)	
					Next interval down

FIG. 3B

Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map
See also: equivalent interval on GB4 map

About This Interval

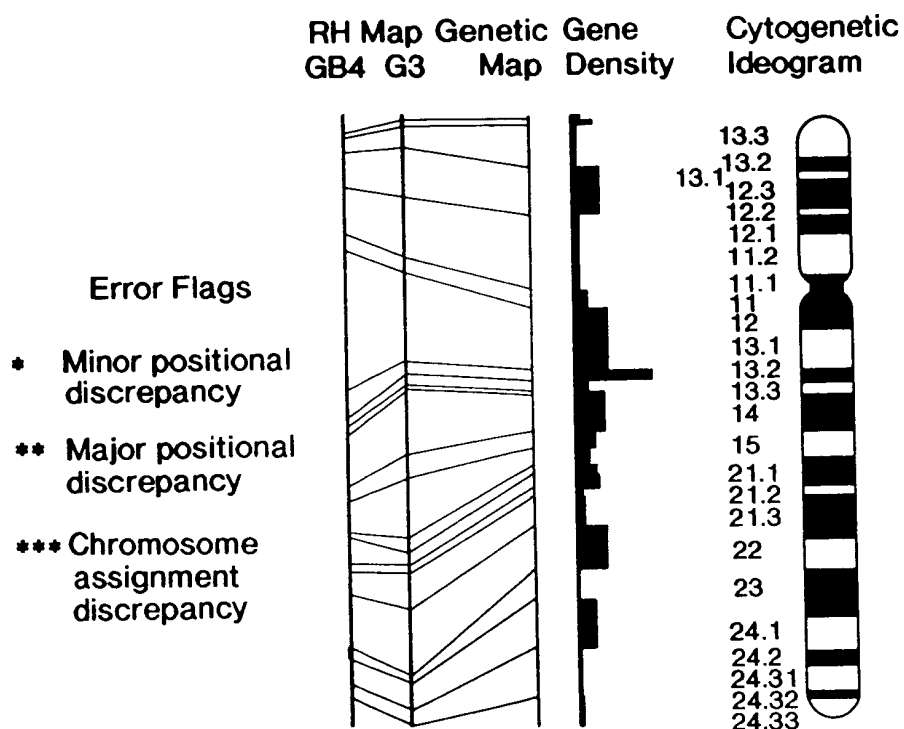
Top of interval: D12S366 (133.8 cM)
 Bottom of interval: D12S340 (147.5 cM)
 Genetic size of bin: 14 cM
 Physical size of bin: 261 cR₁₀₀₀₀

FIG. 3C

					Next interval up
133.8	◆ 5018 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)	
135.1	5047 F	AFMa225xe5	D12S1619	Microsatellite marker AFMa225xe5 (SHGC-20..	
	◆ 5085 F	SHGC-33949	KIAA0262	KIAA0262 gene product	
	◆ 5089 F	SHGC-10488	KIAA0152	KIAA0152 gene product	
	◆ 5093 F	SHGC-10346		Homo sapiens HSPC004 mRNA, complete cds	
	◆ 5098 F	SHGC-13898		Homo sapiens HSPC004 mRNA, complete cds	
137.5	◆ 5163 F	AFM220zf4	D12S321	Microsatellite marker AFM220zf4 (SHGC-212..	
	5199 F	SHGC-11702		ESTs	
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)	
					Next interval down

FIG. 3D

Chromosome 12: D12S340-D12S97



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

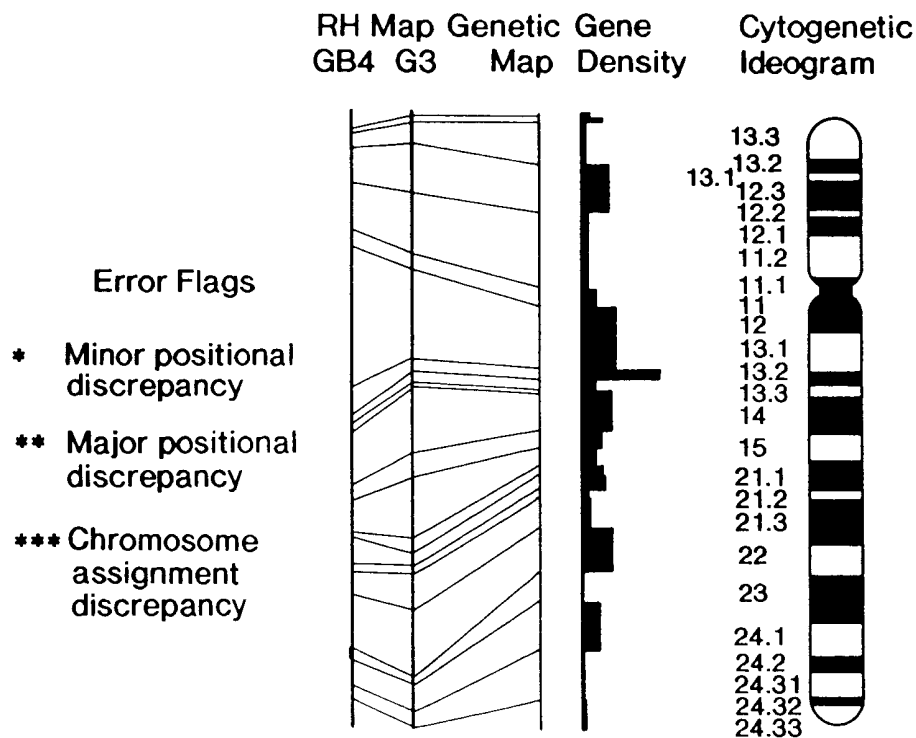
Physical size of bin: 151 cR₁₀₀₀₀

FIG. 3E

					↑ Next interval up
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)	
148.3	5288 F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..	
154.4	5316 F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..	
149.5	5358 F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..	
157.2	5393 F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..	
160.9	◆ 5415 F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..	
160.9	◆ 5430 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6 (SHGC-372)	

FIG. 3F

Chromosome 12: D12S97-qTEL



The interval shown is on the G3 map
 See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S97 (160.9 cM)
 Bottom of interval: chr12_qTEL (169.1 cM)
 Genetic size of bin: 8 cM
 Physical size of bin: ~ 4429 cR₁₀₀₀₀

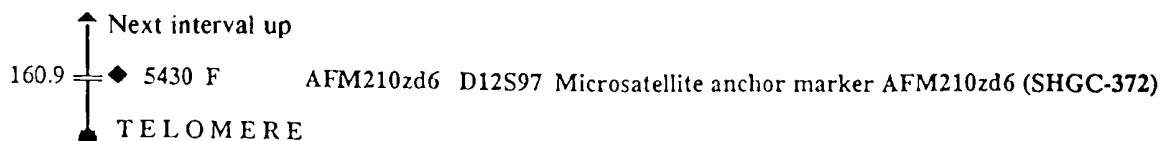


FIG. 3G

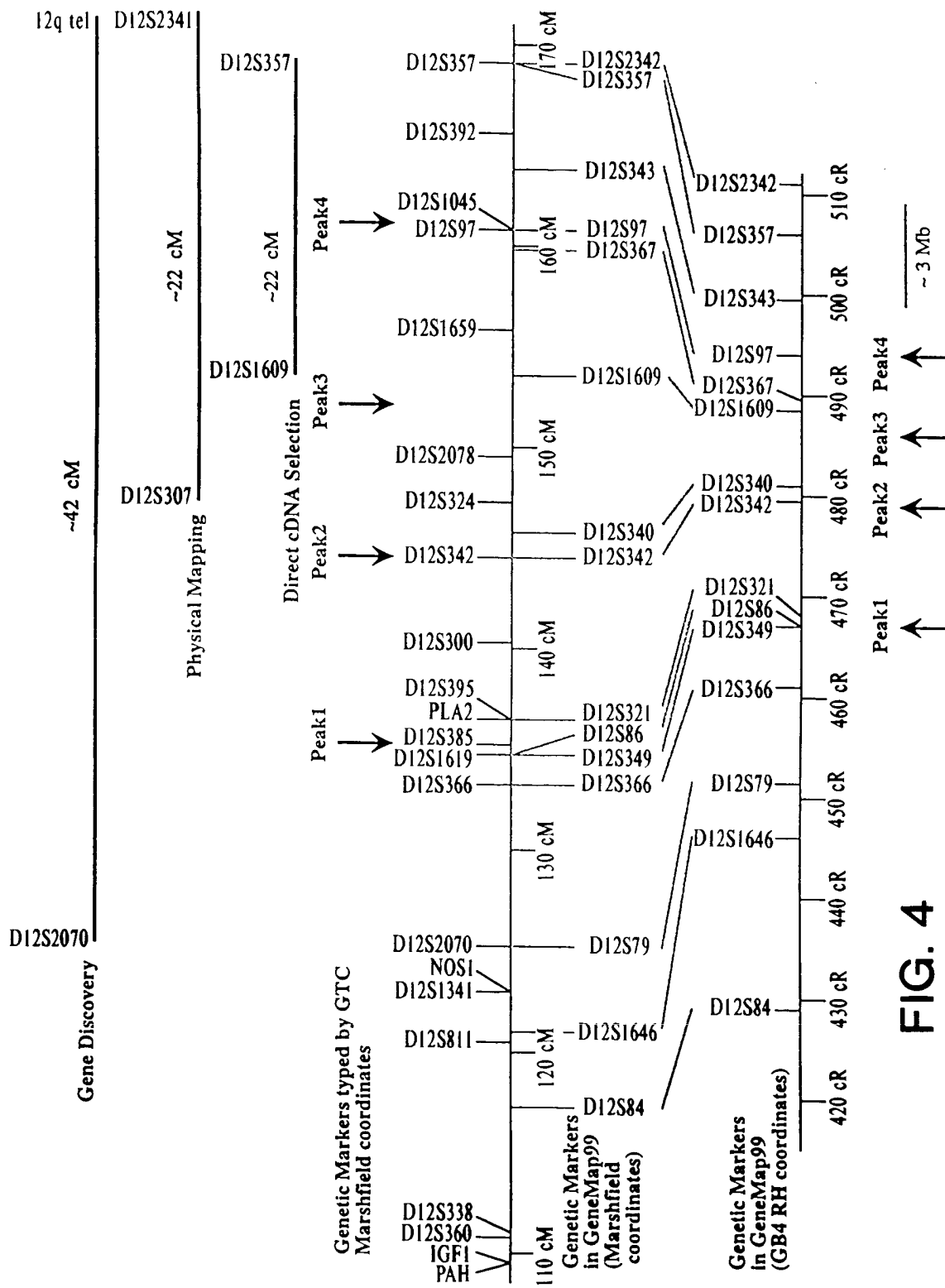


FIG. 4

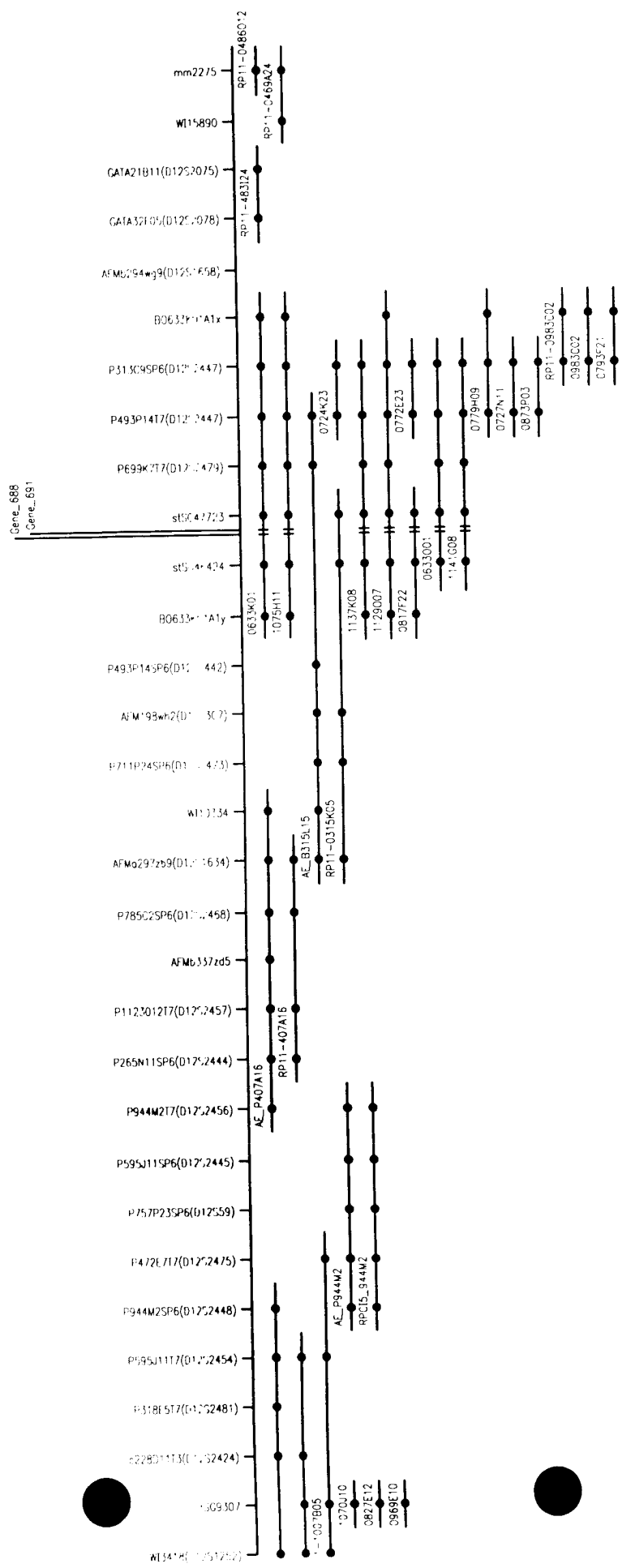


FIG. 5A

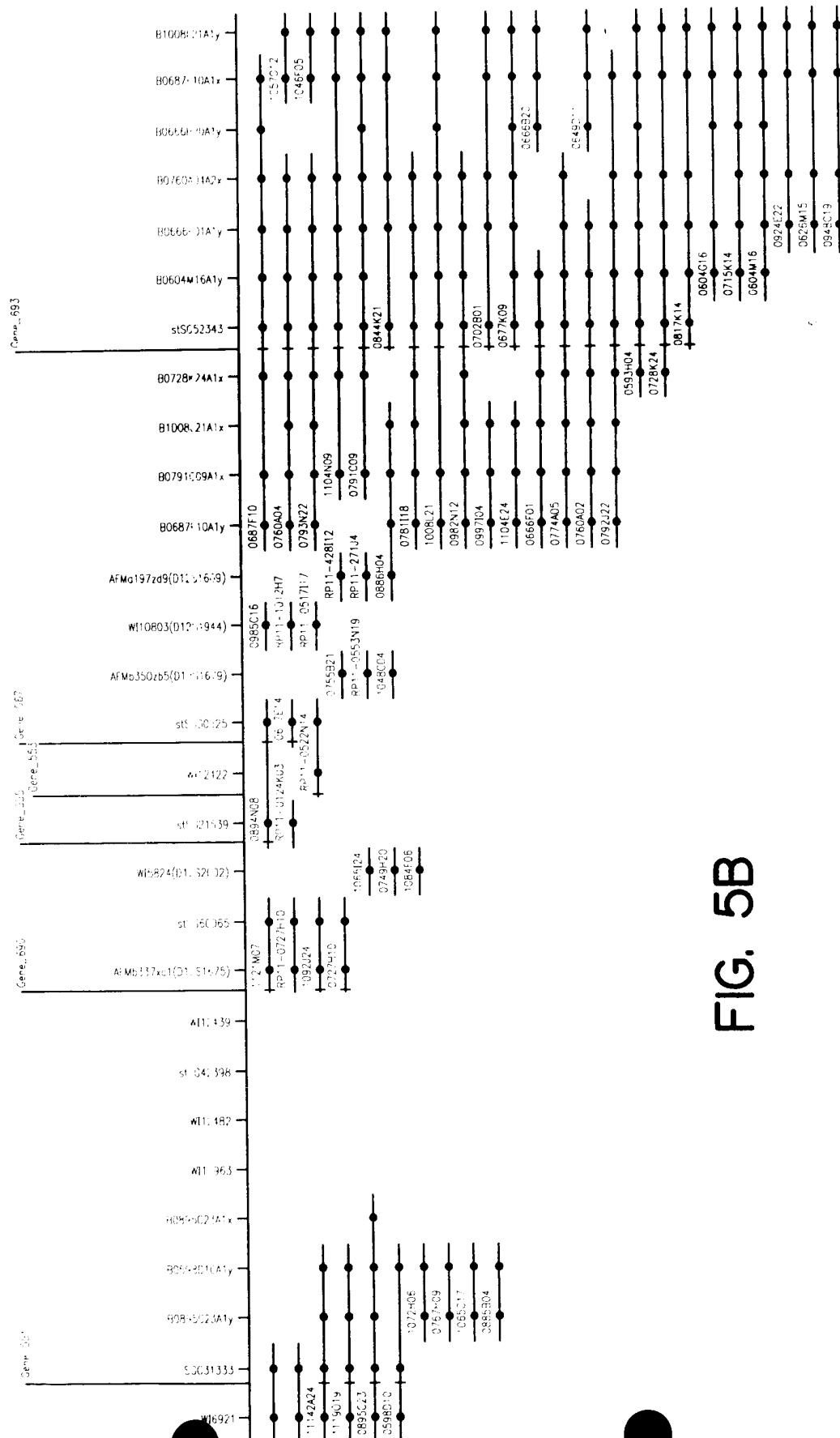
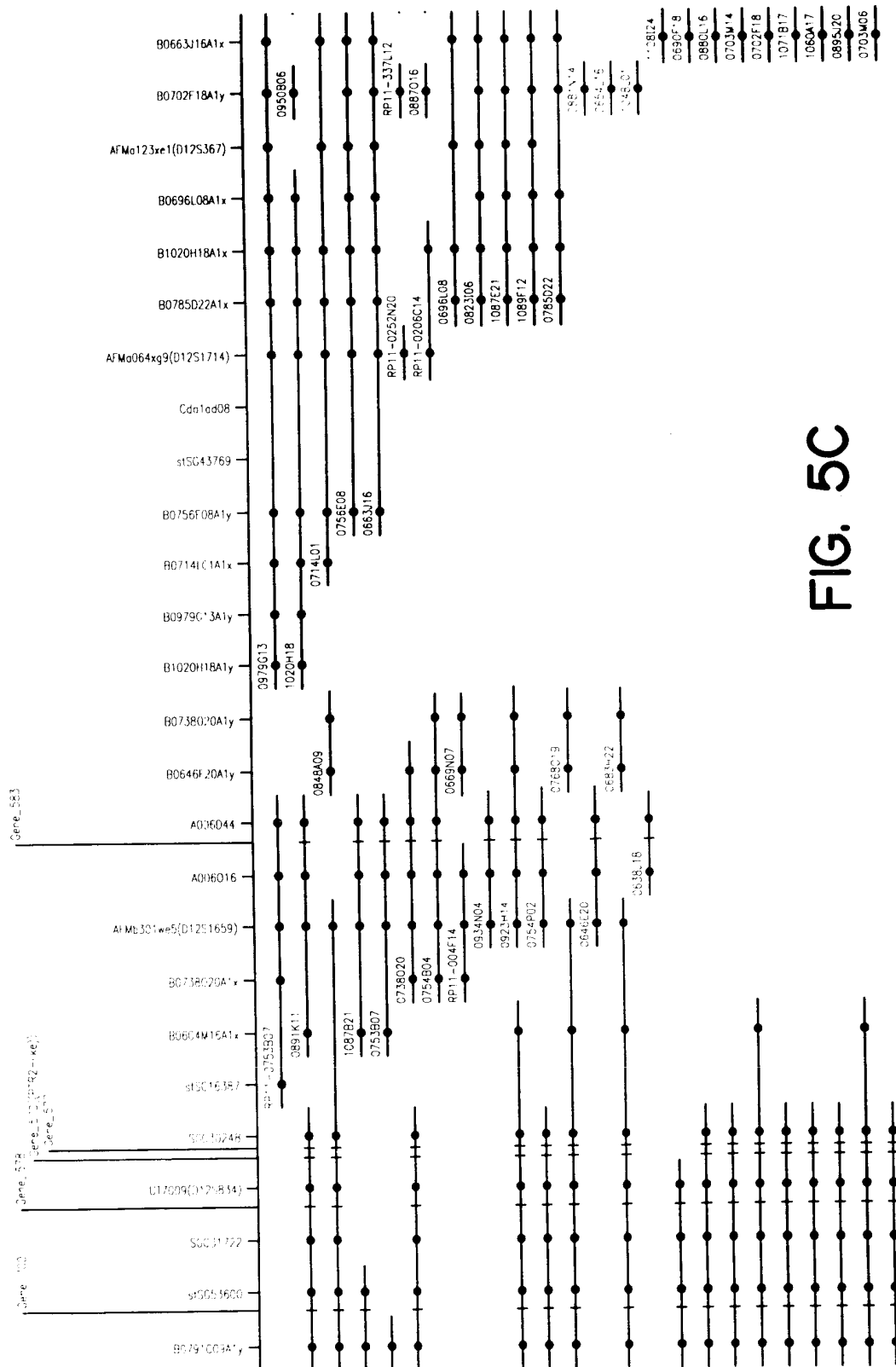


FIG. 5B



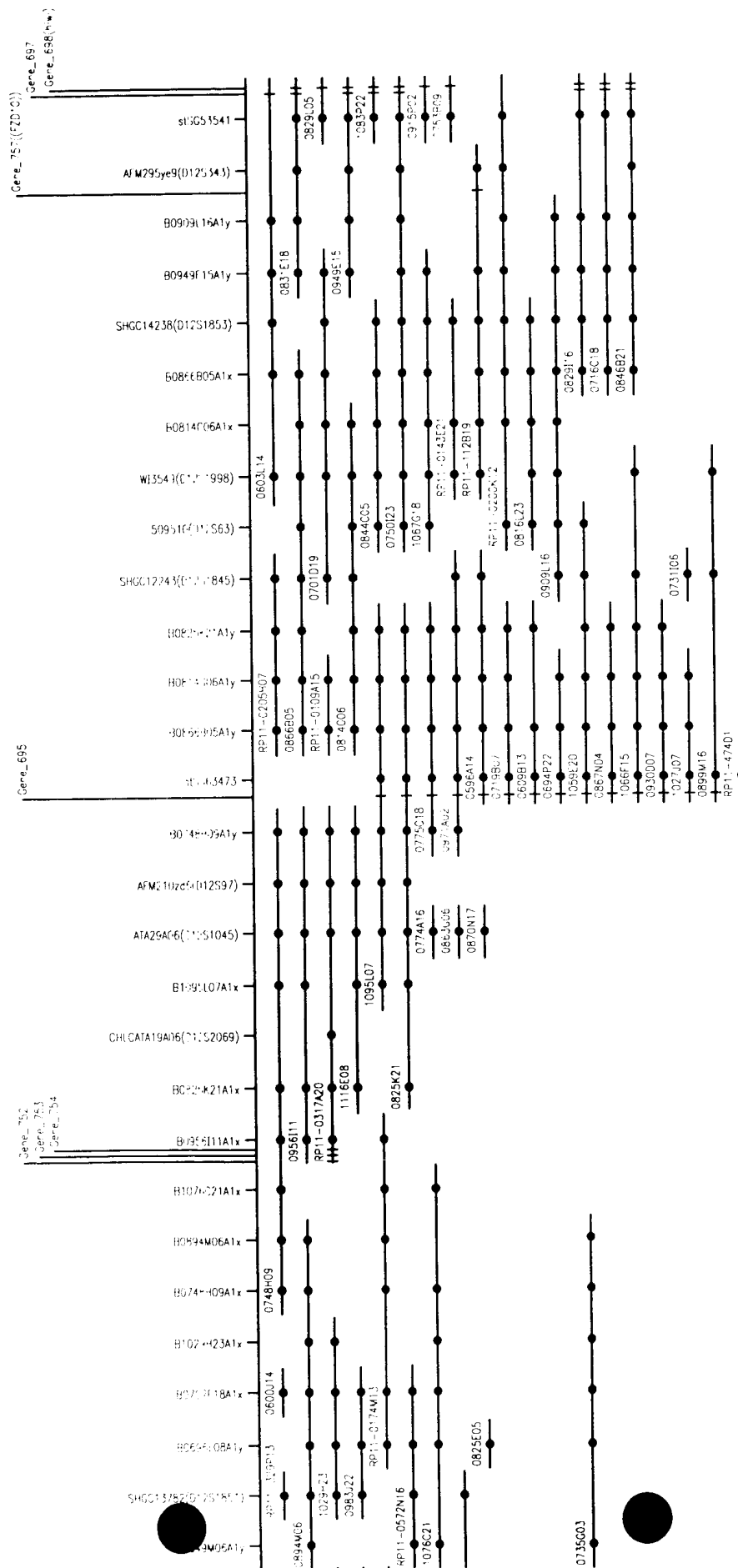
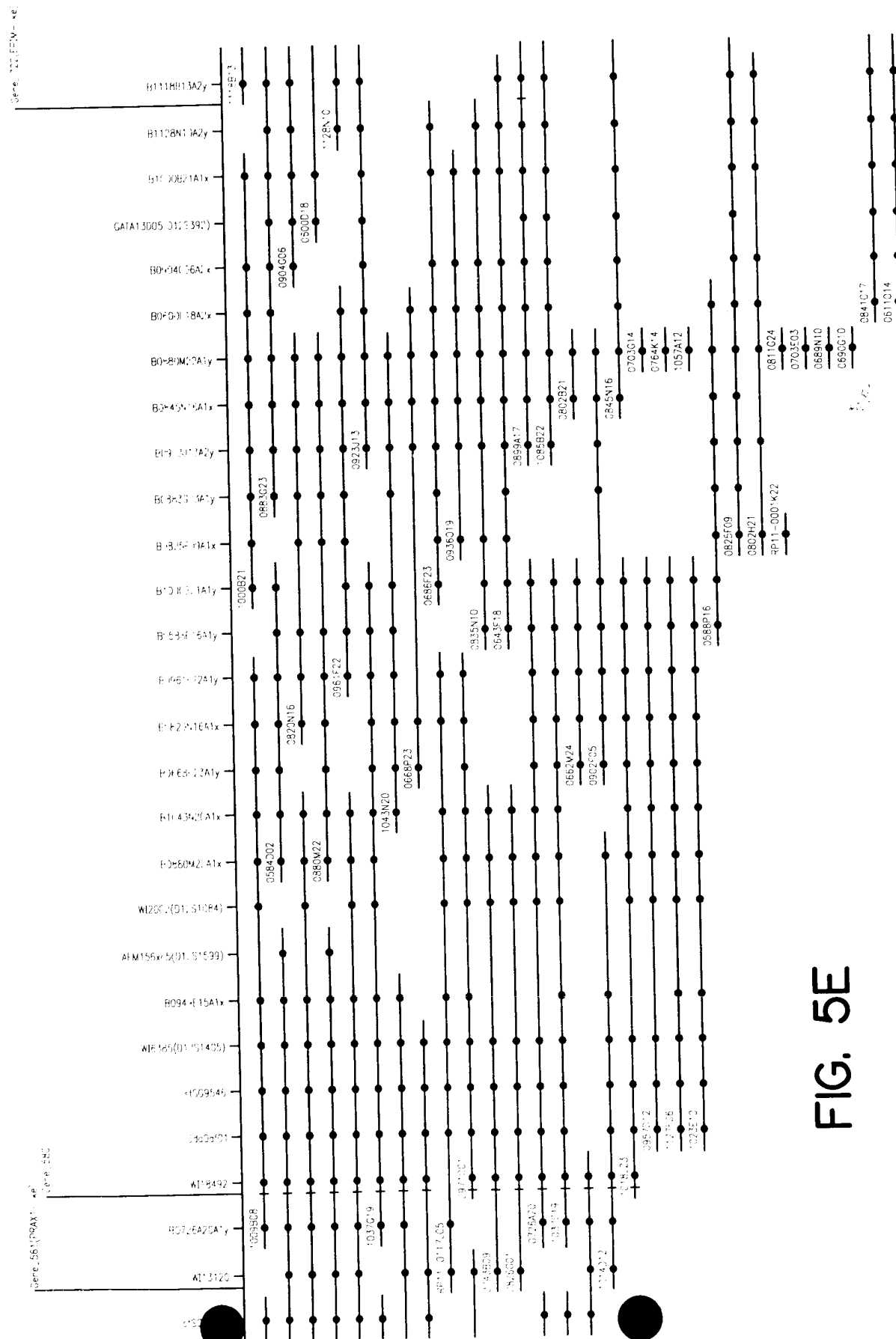
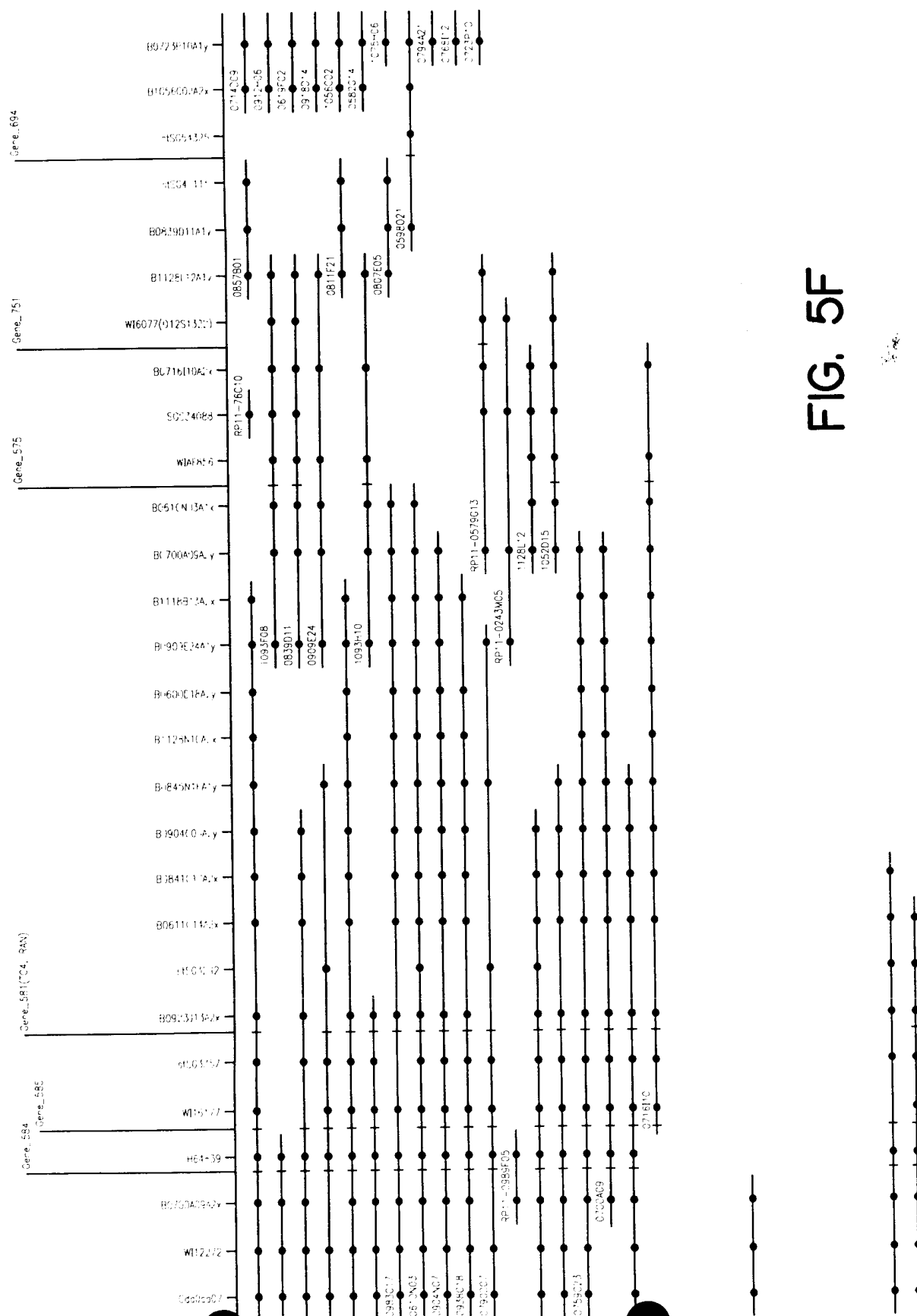
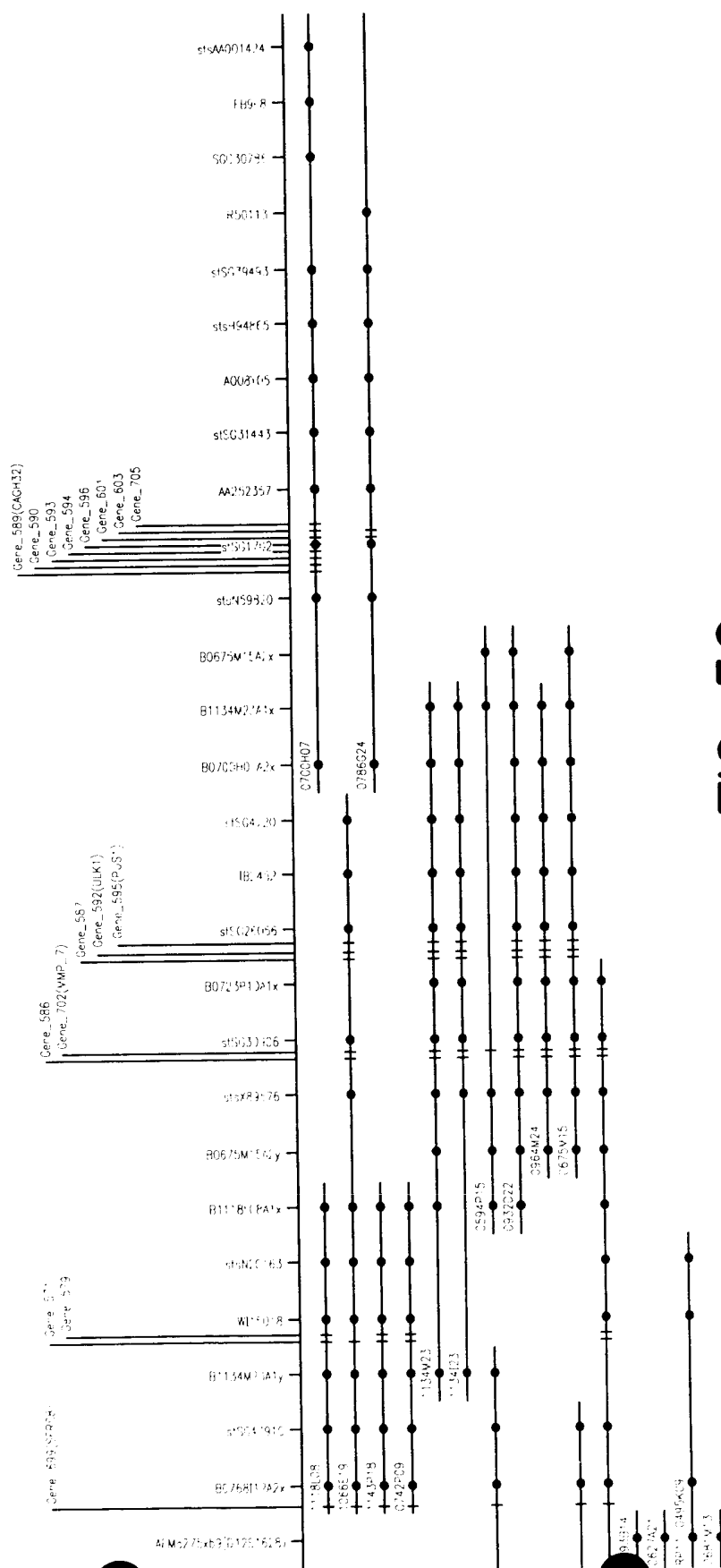
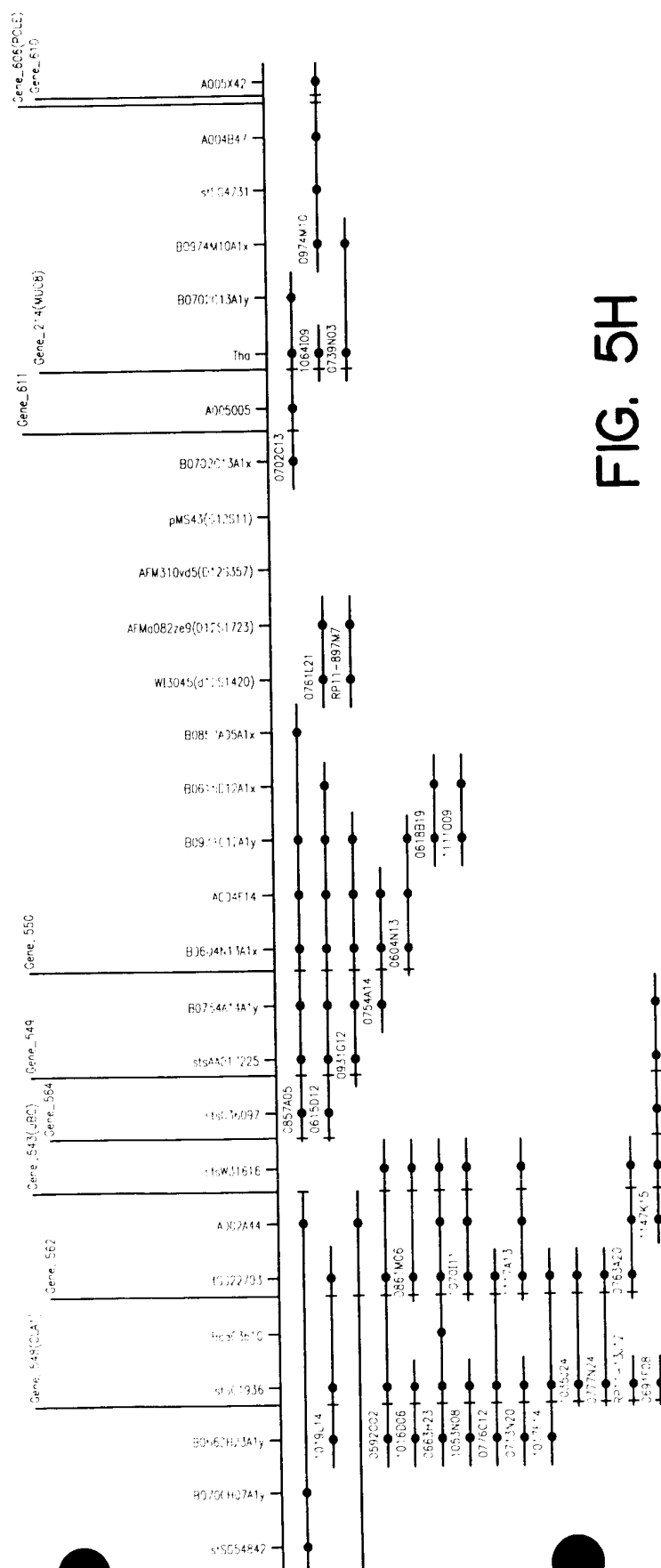


FIG. 5D









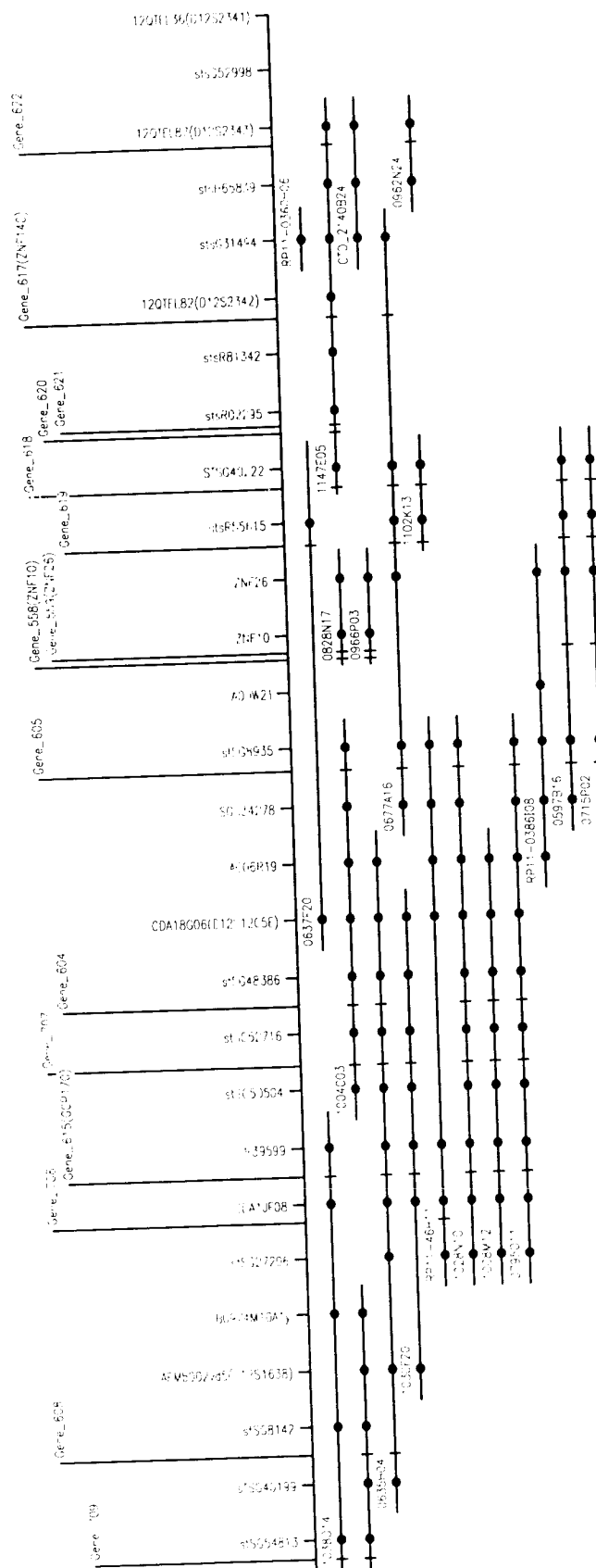
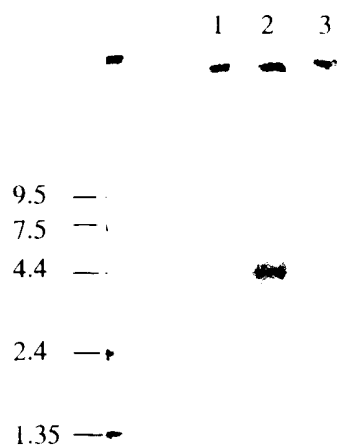


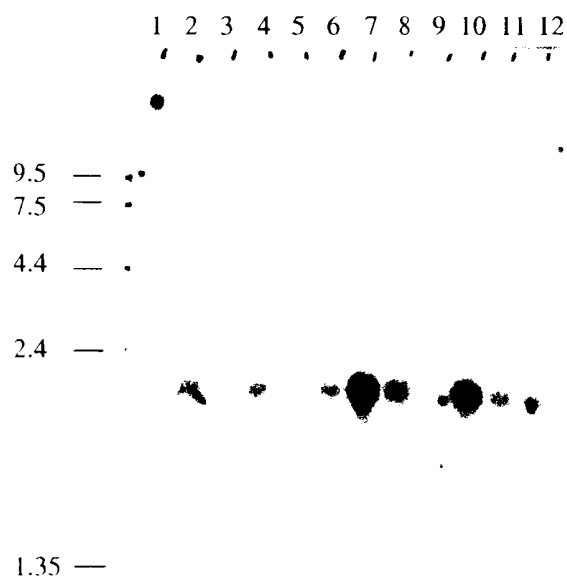
FIG. 51

Gene 214



1. Lymphoblastoid cell line
2. Lung
3. Trachea

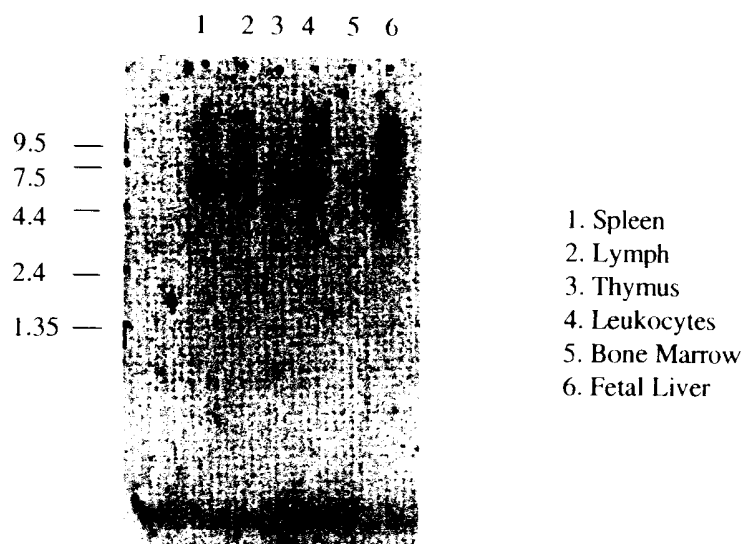
Gene 436



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6A

Gene 454



Gene 515

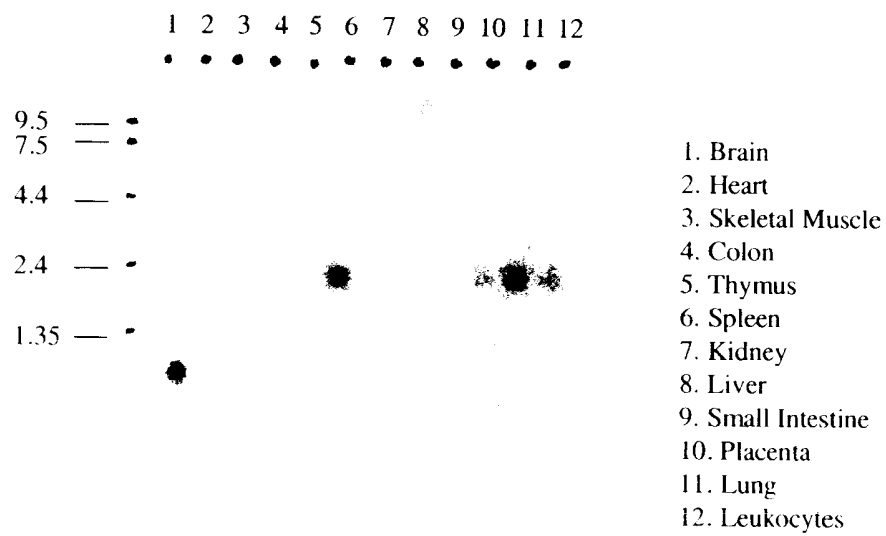
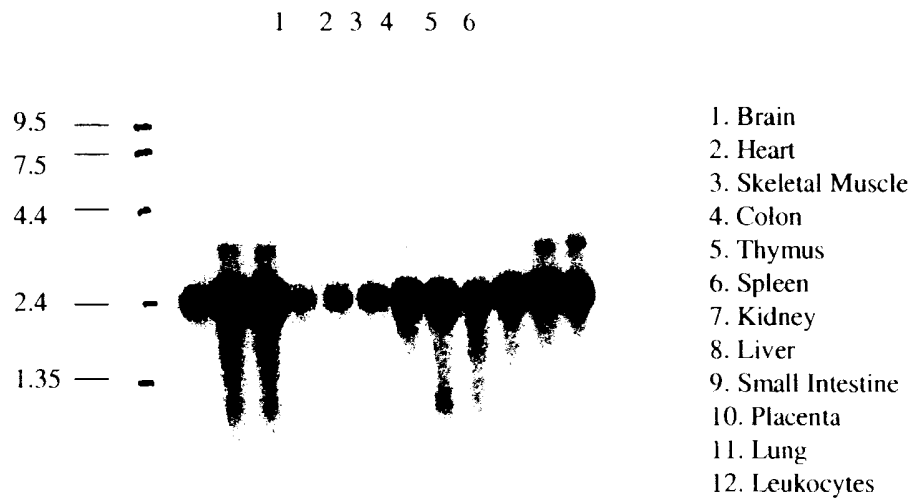


FIG. 6B

Gene 543

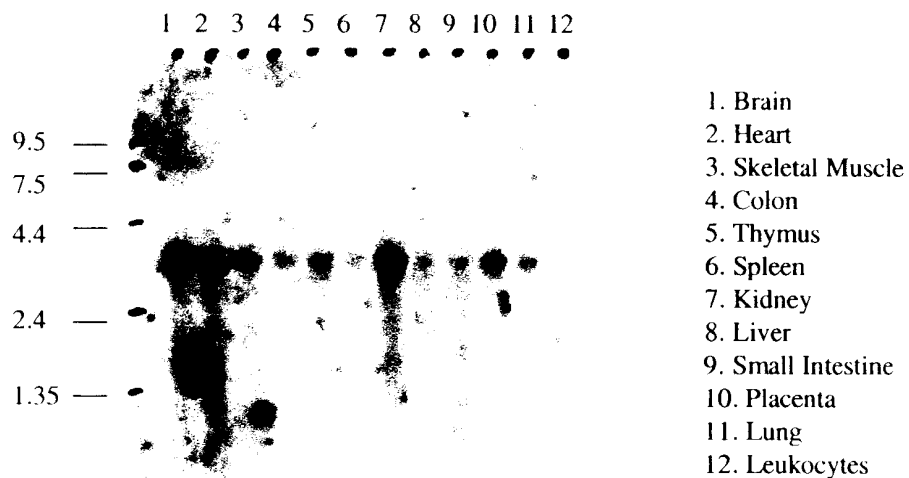


Gene 548



FIG. 6C

Gene 550



Gene 561

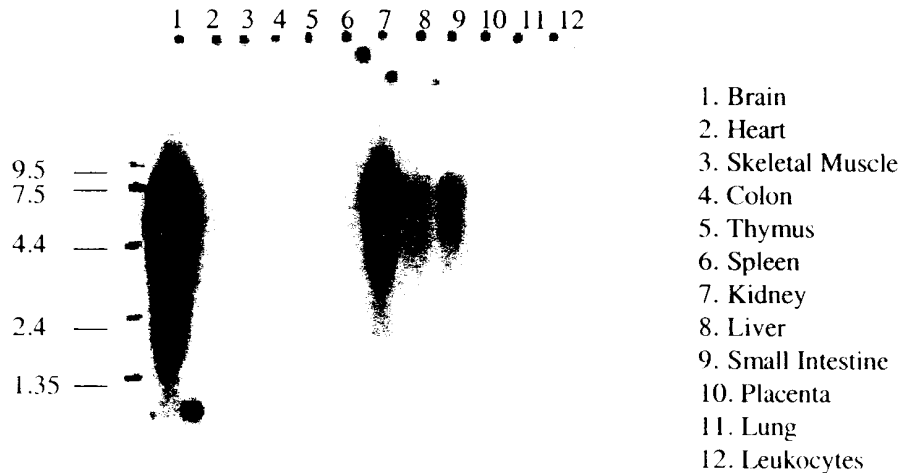


FIG. 6D

Gene 564



Gene 570

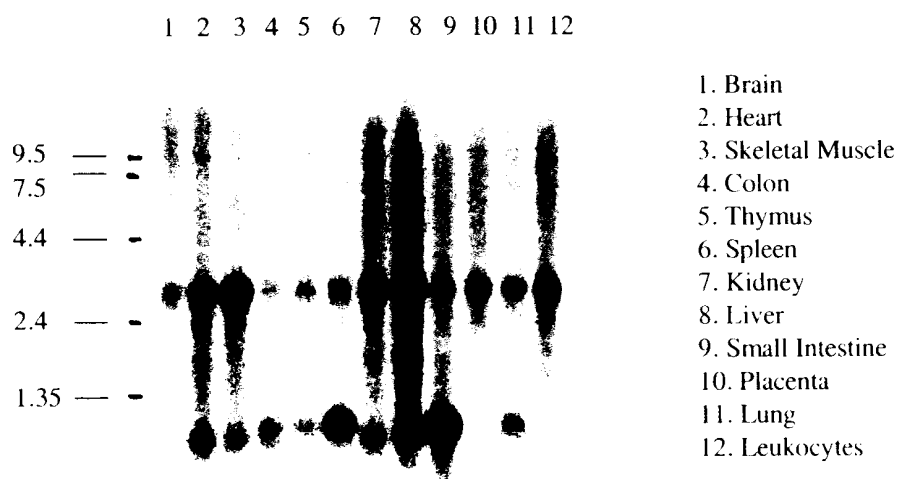
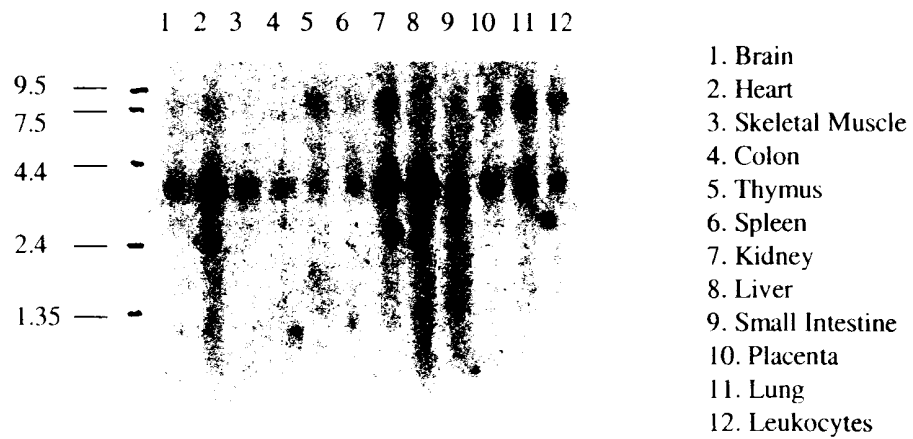


FIG. 6E

Gene 576



Gene 577

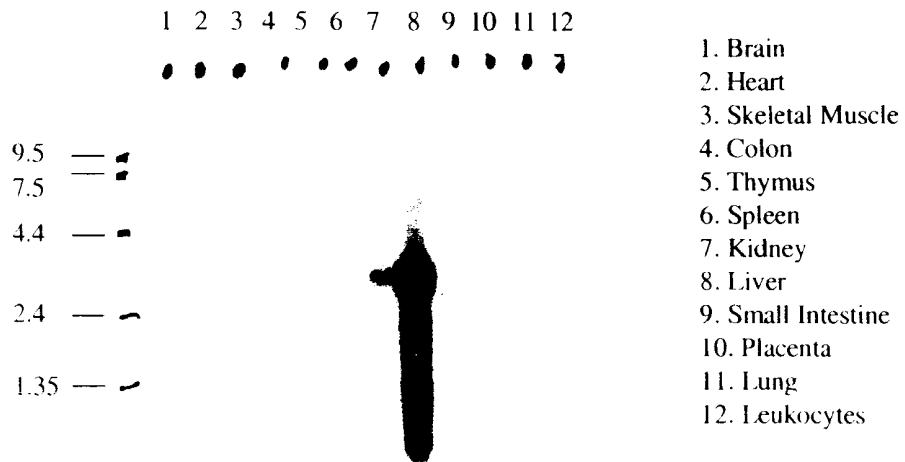
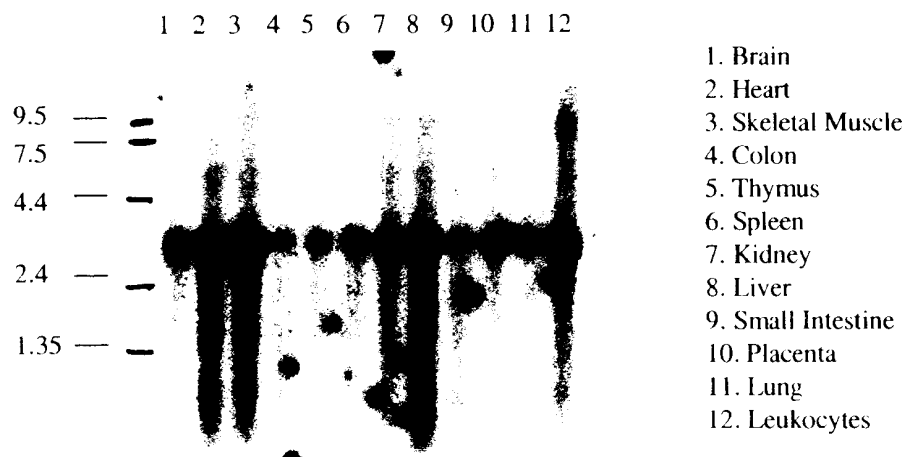


FIG. 6F

Gene 578



Gene 579

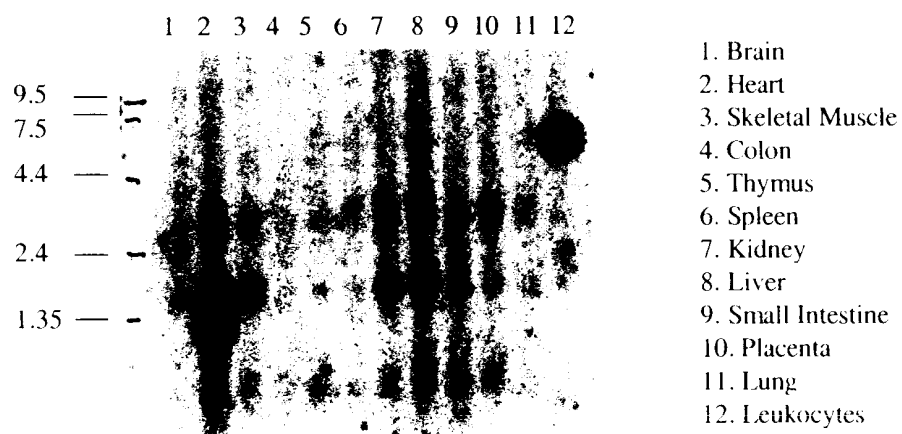
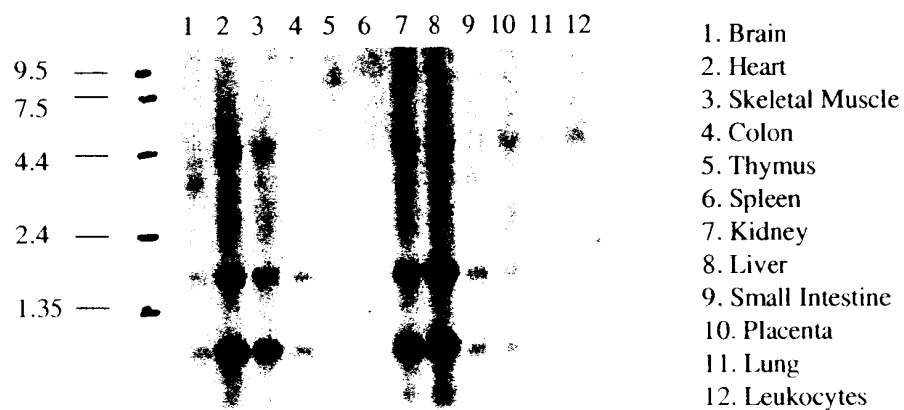


FIG. 6G

Gene 580



Gene 581

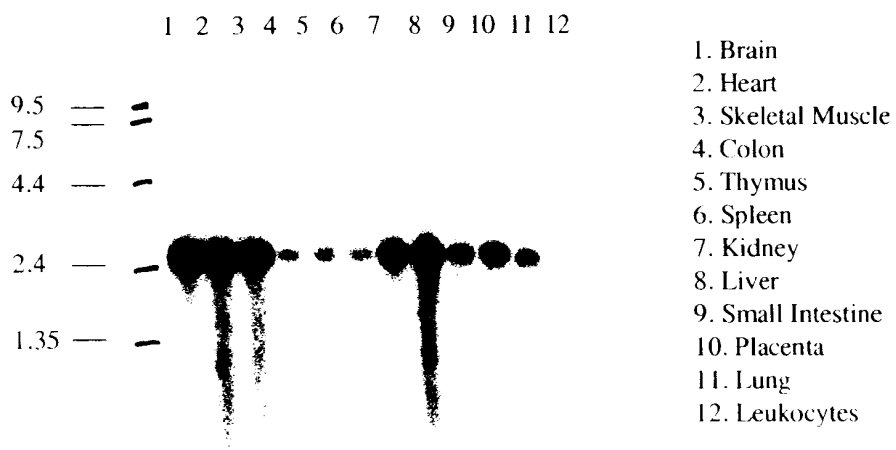
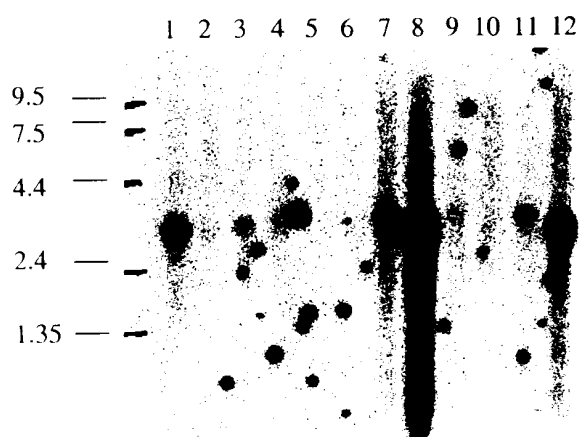


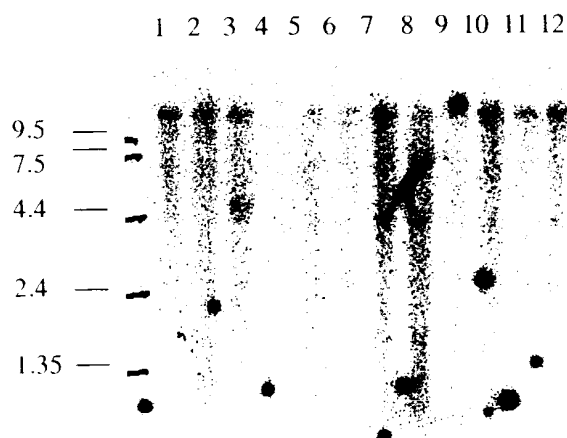
FIG. 6H

Gene 583



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

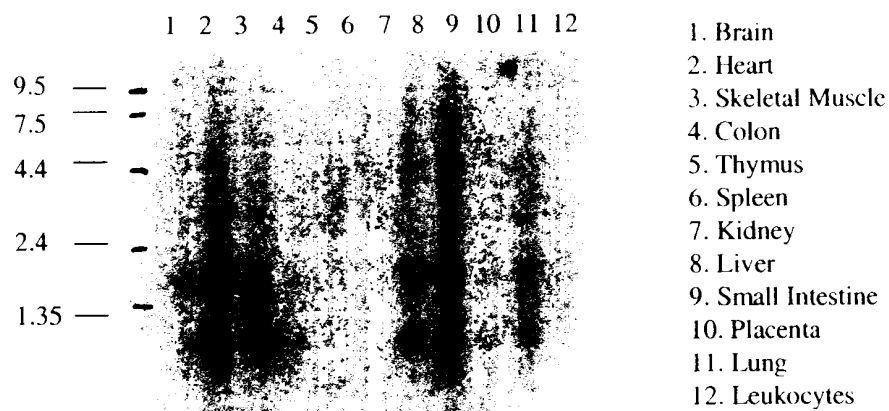
Gene 589



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6I

Gene 590



Gene 592

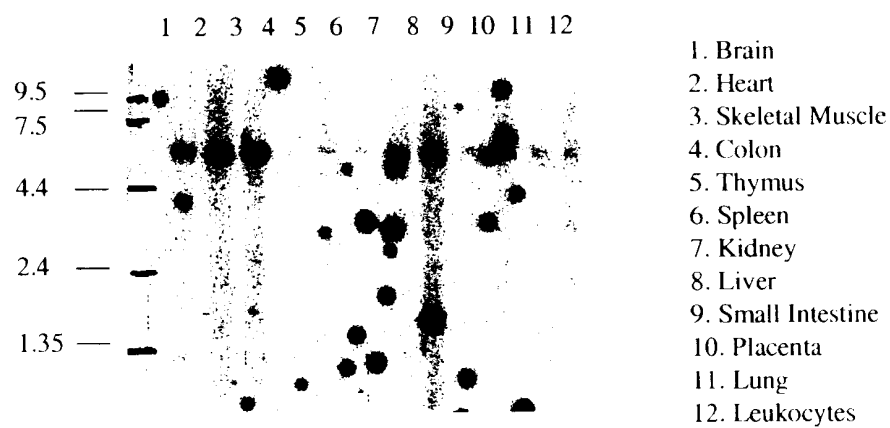
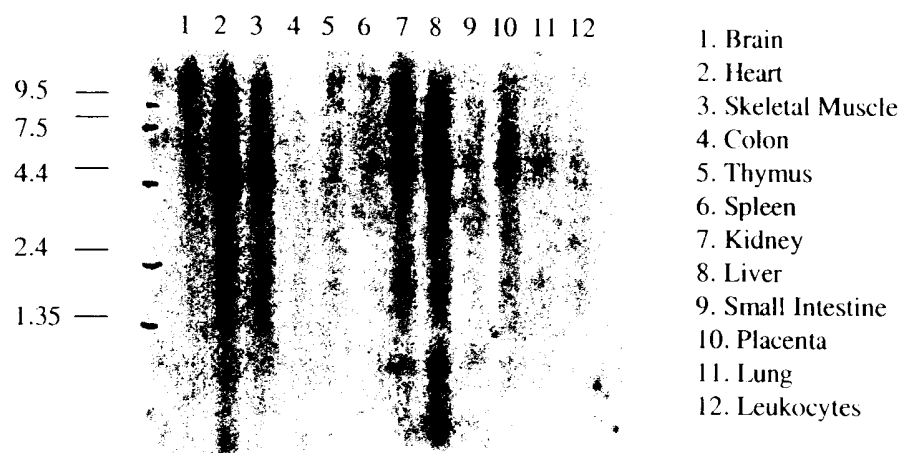


FIG. 6J

Gene 594



Gene 595

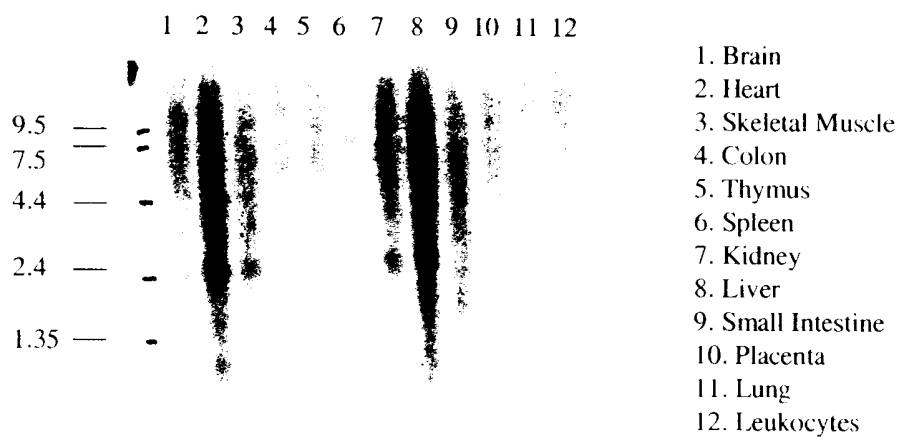
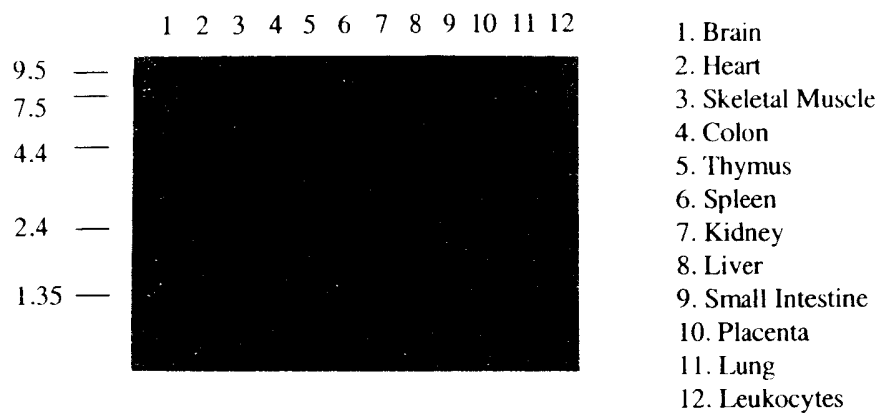


FIG. 6K

Gene 596



Gene 604

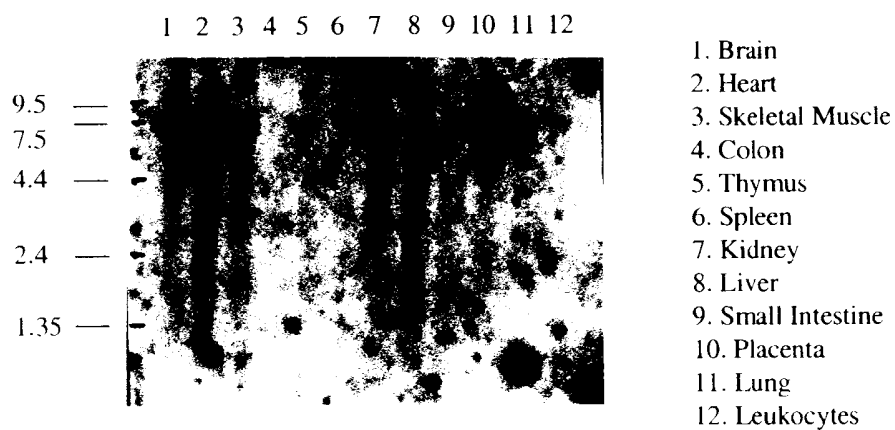
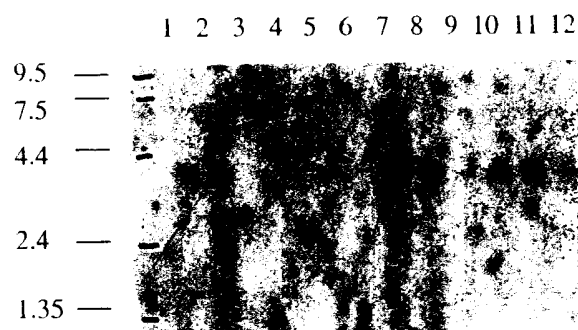


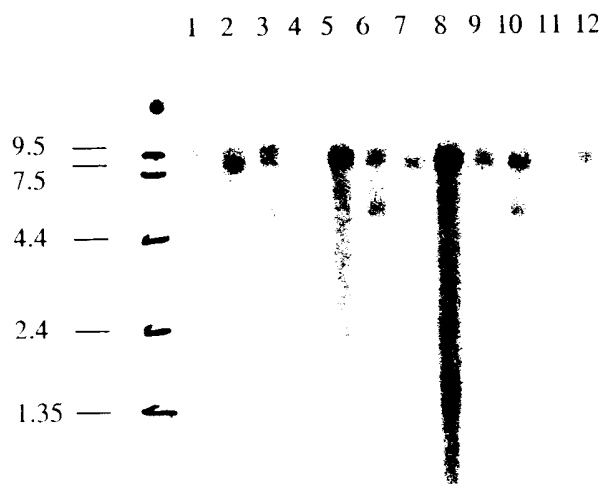
FIG. 6L

Gene 605



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

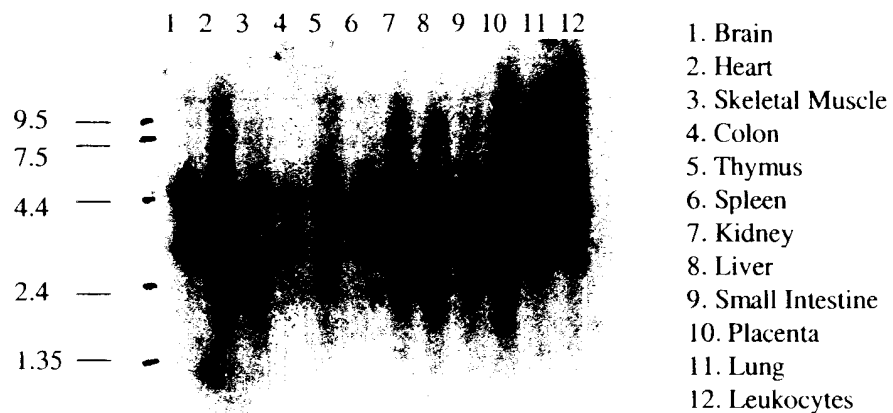
Gene 606



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6M

Gene 608



Gene 611

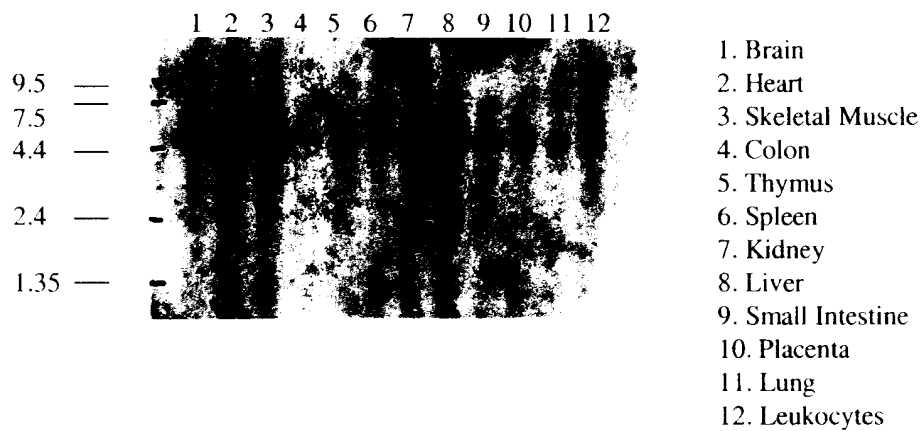
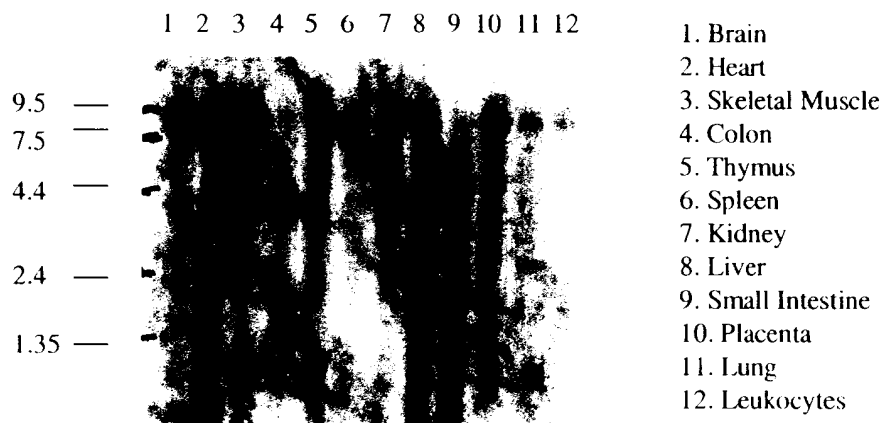


FIG. 6N

Gene 615



Gene 617

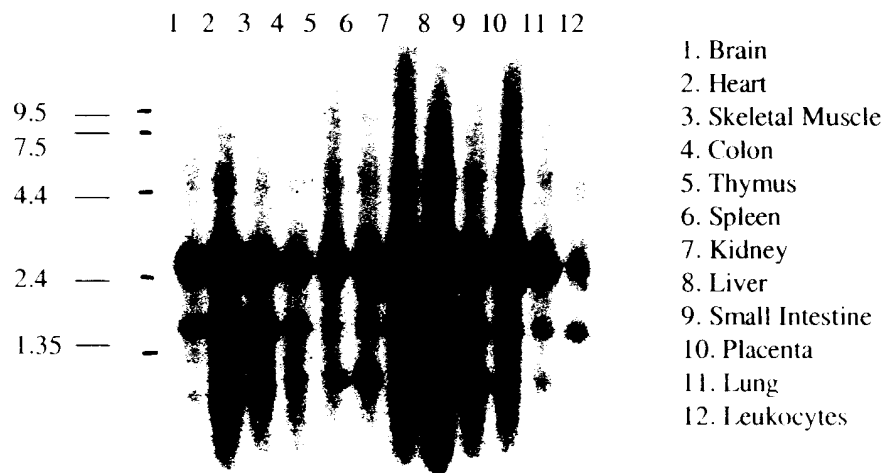
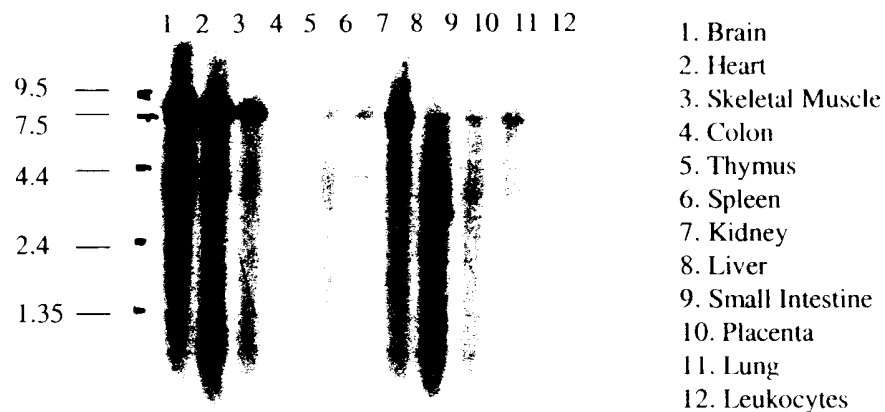


FIG. 60

Gene 618



Gene 619

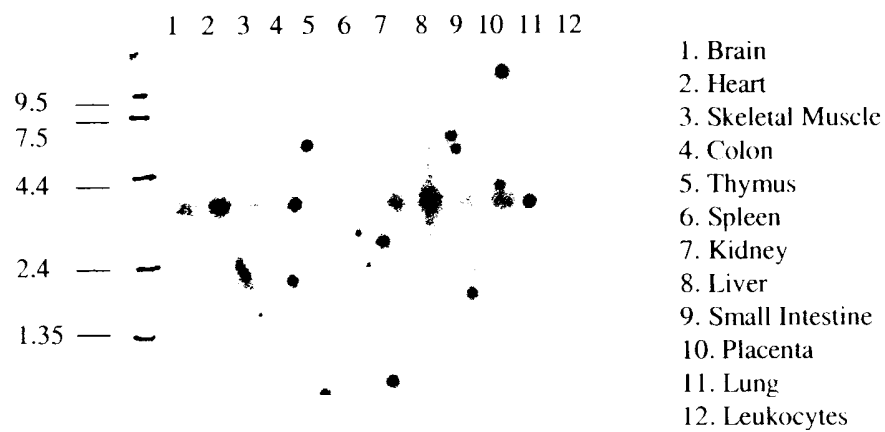
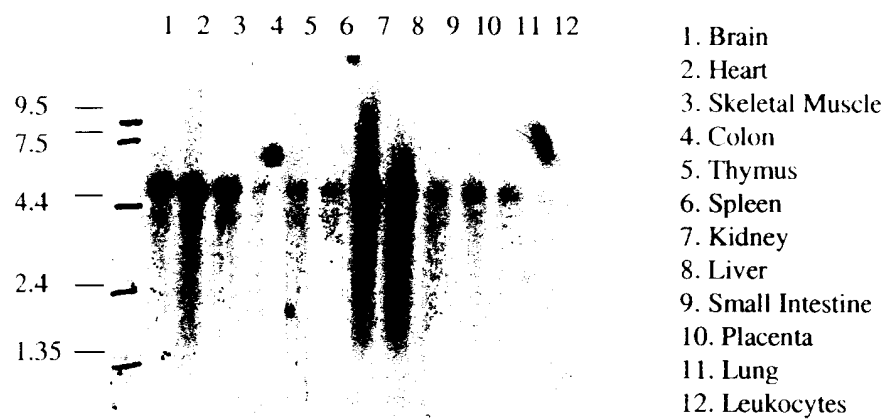


FIG. 6P

Gene 621



Gene 693

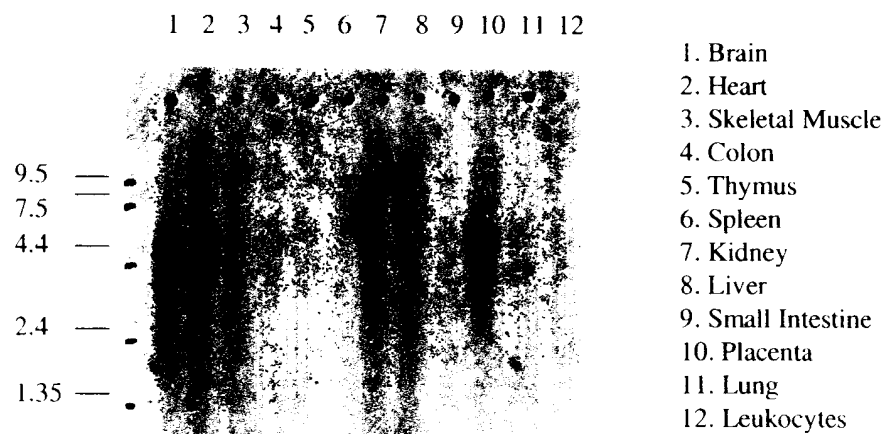
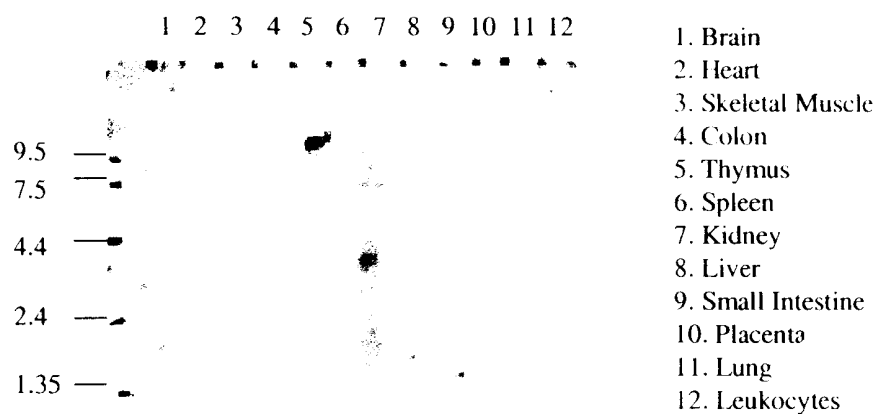


FIG. 6Q

Gene 698



Gene 699

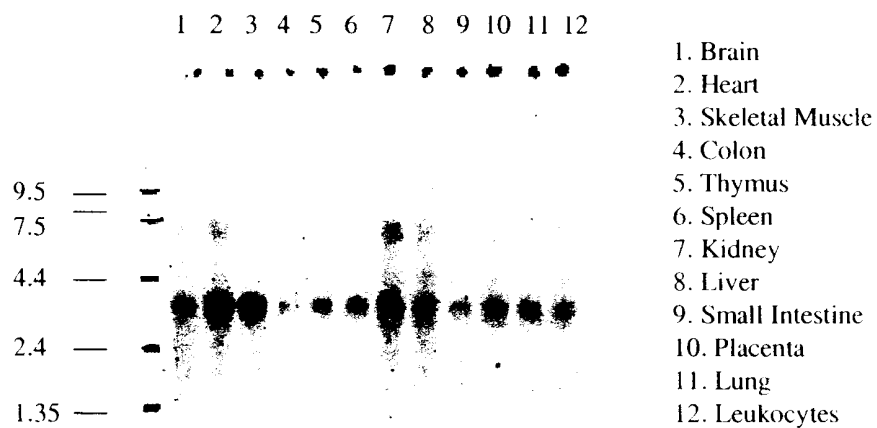
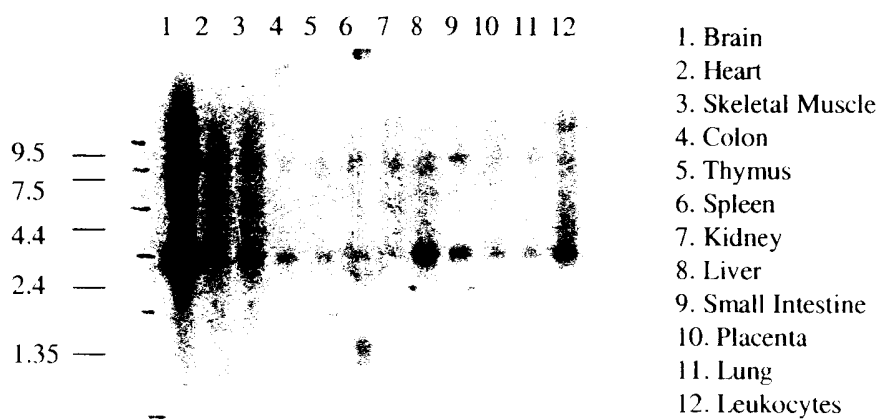


FIG. 6R

Gene 702

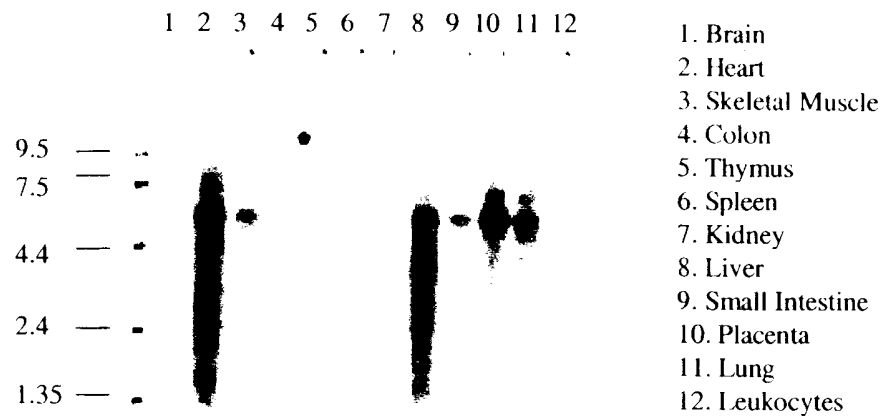


Gene 722



FIG. 6S

Gene 751



Gene 756

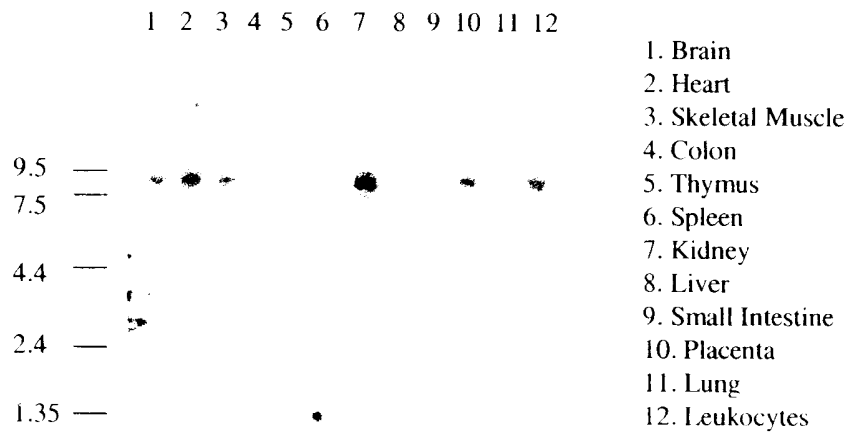
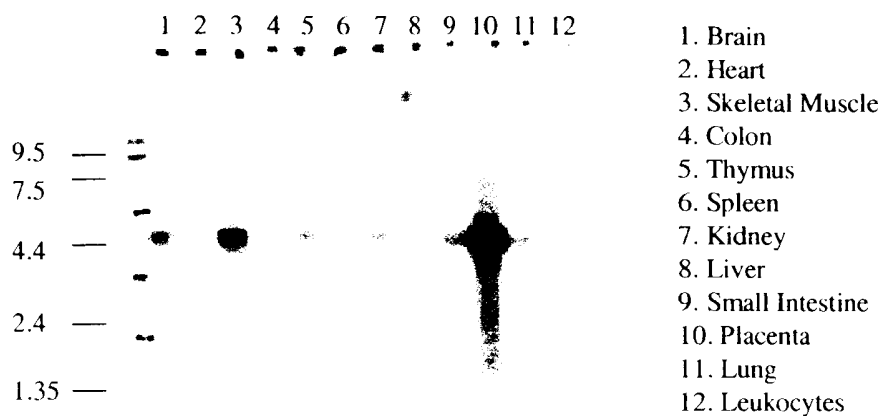


FIG. 6T

Gene 757



Gene 848

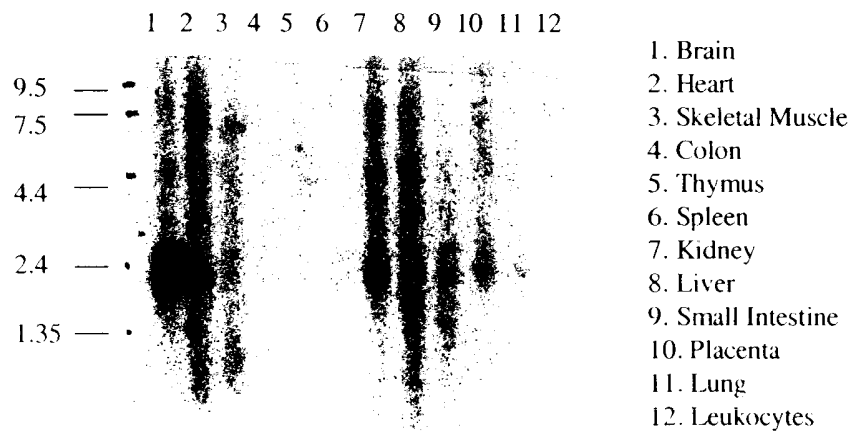


FIG. 6U

10	30	50
GCTTGCTGTGGCCCTGTCAGGAAGAGTAGAGCTCTGGTCCAGCTCCGCGCAGGGAGGGAG		
70	90	110
GCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTTCCAGTATGAGACGAACAAA MetProAlaCysCysSerCysSerAspValPheGlnTyrGluThrAsnLys		
130	150	170
GTCACCTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTTCCACGTGATCATC ValThrArgIleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIle		
190	210	230
TTTTCTACGTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTG PheSerTyrValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProVal		
250	270	290
ATCAGTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGAGATCGTGGAG IleSerSerValHisThrLysValLysGlyIleAlaGluValLysGluGluIleValGlu		
310	330	350
AATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTGACACCGCAGACTACACCTTCCCTTTG AsnGlyValLysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeu		
370	390	410
CAGGGGAACCTCTTCTTCGTGATGACAACTTTCTCAAACAGAAGGCCAAGAGCAGCGG GlnGlyAsnSerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluGlnArg		
430	450	470
TTGTGTCCCGAGTATCCCACCCGCAGGACGCTCTGTTCTCTGACCGAGGTTGTAAAAAG LeuCysProGluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLys		
490	510	530
GGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCGGAAGGTGTGTAGTGCATGAAGGG GlyTrpMetAspProGlnSerLysGlyIleGlnThrGlyArgCysValValHisGluGly		
550	570	590

FIG. 7A

AACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCC
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluGluAlaPro

610 630 650
CGGCCTGCTCTCTTGAACAGTGCCGAAAACCTCACTGTGCTCATCAAGAACAATATCGAC
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

670 690 710
TTCCCCGGCCACAACCTACACCACGAGAAACATCCTGCCAGGTTTAAACATCACTTGTACC
PheProGlyHisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

730 750 770
TTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAGGAGACATCTTCCGAGAA
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

790 810 830
ACAGGCGATAATTTTTTCAGATGTGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTAC
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

850 870 890
TGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCGTCCCAAATACAGTTTCCGTCGC
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

910 930 950
CTTGACGACAAGACCACCAACGTGTCCTTGTACCCTGGCTACAACCTCAGATACGCCAAG
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

970 990 1010
TACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGATCCGTTTT
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

1030 1050 1070
GACATCCTGGTTTTTGGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATC
AspIleLeuValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIle

1090 1110 1130
GGCTCAACCTCTCCTACTTCGGTCTGGCCACTGTGTTTCATCGACTTCCTCATCGACACT
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr

1150	1170	1190
TACTCCAGTAACTGCTGTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCAGCCCTGT TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys		
1210	1230	1250
GTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTCCATTGTGGAGCCAAAGCCGACA ValValAsnGluTyrTyrTyrArgLysLysCysGluSerIleValGluProLysProThr		
1270	1290	1310
TTAAAGTATGTGTCCTTTGTGGATGAATCCCACATTAGGATGGTGAACCAGCAGCTACTA LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu		
1330	1350	1370
GGGAGAAGTTTGCAAGATGTCAAGGGCCAAGAAGTCCCAAGACCTGCGATGGACTTCACA GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr		
1390	1410	1430
GATTTGTCCAGGCTGCCCTTGGCCCTCCATGACACACCCCGATTCTGGACAACCAGAG AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu		
1450	1470	1490
GAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCC [~] CGTCTGGTGC GluIle <u>Gln</u> LeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys		
1510	1530	1550
CAGTGTGGAAGATGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTG GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGlu <u>Glu</u> Leu		
1570	1590	1610
TGCTGCCCGAAAAAGCCGGGGGCTGCATCACCACTCAGAGCTGTTTCAGGAAGCTGGTC CysCysArgLysLysProGlyAlaCysIleThrThrSerGluLeuPheArgLysLeuVal		
1630	1650	1670
CTGTCCAGACACGTCCTGCAGTTCCTCTGCTCTACCAAGAGCCCTTGCTGGCGCTGGAT LeuSerArgHisValLeuGlnPheLeuLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp		
1690	1710	1730

FIG. 7C

GTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGTGCTACGCCACCTGGCGC
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750 1770 1790
TTCGGCTCCCAGGACATGGCTGACTTTGCCATCCTGCCCAGCTGCTGCCGCTGGAGGATC
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810 1830 1850
CGGAAAGAGTTTCCAAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAGTCCTTACTGAAGC
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870 1890 1910
CAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTTGGGAGGCCGAGGCAGGCAGATCA

1930 1950 1970
CCTGAGATCGGGAGTTGGAGACCCGCTGGCTAACAAGGCGAAATCCTGTCTGTACTAA

1990 2010 2030
AATACAAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050 2070 2090
GAGGCACAAGAATCACTTGAACCCGGGAGGCAGAGGTTGTAGTGAGCCCAGATTGTGCCA

2110 2130 2150
CTGCTCTCCAGCCTGGGAGGCACAGCAAAGTGTCCCAAAAAAAAAAAAAAGAGTCCTTAC

2170 2190 2210
CAATAGCAGGGGCTGCAGTAGCCATGTTAACATGACATTTACCAGCAACTTGAACCTCAC

2230 2250 2270
CTGCAAAGCTCTGTGGCCACATTTTCAGCCAAAGGGAAATATGCTTTCATCTTCTGTTGC

2290 2310 2330
TCTCTGTGTCTGAGAGCAAAGTGACCTGGTTAAACAAACCAGAATCCCTCTACATGGACT

2350 2370 2390

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGTGACCCTA
 2410 2430 2450
 GGCTCTCACCTCTGTGCCTCTGTCTCCTTGTTGCCCACTACTATCTCAGAGATATTGT
 2470 2490 2510
 GAGGACAAATTGAGACAGTGCACATGAAGTGTCTTTTAATGTGTAAAGATCTACATGAAT
 2530 2550 2570
 GCAAAACATTTTATTATGAGGTCAGACTAGGATAATGTCCAATAAAAAACAAACCCTTTT
 2590 2610 2630
 CATCCTGGCTGGAGAATGTGGAGAACTAAAGCTGGCCACAAATTCTTTGAACTCAAGTC
 2650 2670 2690
 CCCCAGACCTAAGGGTTTTATCTCCTCCCCTTGAATATGGGTGGCTCTGATTGCTTTAT
 2710 2730 2750
 CCAAAAGTGGAAGTGACATTGTGTCAGTTTCAGATCCTGATCTTAAGAGGCTGACAGCTT
 2770 2790 2810
 CTACTTGCTGTCCCTTGGAAGTCTTGCTATCGGGGAAGCCAGACGCCATTTAAAGTCTG
 2830 2850 2870
 CCTATCCTGGCCAGGTGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGACCAAGG
 2890 2910 2930
 CGGGCGGATCACTTAAAGTCAGGAGTCCAAGACCAGACTCGCCAAACATGGTGAAACCGTA
 2950 2970 2990
 TCTCTAATAAAAAATACAAAAATTAGCTGGGCATGGTGCGGGCACCTGTAGTCCTAGCTAT
 3010 3030 3050
 CAAGAGGCTGAGACAGGAGAAACACTTGAACCTGGGAGGTGGAGGTTGCATTGAGCTGAG

FIG. 7E

3070	3090	3110
ATCGTGCCACTGCACTCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAA		
3130	3150	3170
AAAAGAAAAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCAAGCA		
3190	3210	3230
GTCACGTGGACAGTGCCTGACCAGCCCCAGCTTTCAAGCCATCCAAGCCCAGTCACCAA		
3250	3270	3290
CATGAGAGAGAAGAAGCCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATACCGC		
3310	3330	3350
ATGATACATCCCAAGTGAGAACTGCCCCATAAATCCAGAAAACCACATTGCTATCTTAAG		
3370	3390	3410
TCCCTAAGTTTGGGGCTTATTTGTTCCACAGCAACAGGTAAGTGAACAGAGGGCAAGCC		
3430	3450	3470
TGATGAATGGGCACACAGACTCAGCCCATACCTTCCCTGGTTCTAATGTTCTCAGGGAGC		
3490	3510	3530
CCGGACCAACCCTGGGAGCCTCAGGAAGTTAGGTTTCCACTGGACAGTTCTAGAAGGGCT		
3550	3570	3590
ATAGACCAAATCAGGTAAGTACCAGACCAGCCTTGGAATCTATCAAATCTAACTGCTGA		
3610	3630	3650
GCTACCCAGTGCATTCCGATCCTCATCACAATTCTTTGACTGAAGGCCGGGCGTGGTGCC		
3670	3690	3710
TCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTCAGGA		

FIG. 7F

3730	3750	3770
GTTTCGAGACCAGCCTGGCCAACATGGTGAGACCCTGTCTCTACTAAGAATACAAAATTA		
3790	3810	3830
GGTGGGGTGGCGGTGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATC		
3850	3870	3890
TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAGTGCCACTGCACTCCAGCCT		
3910	3930	3950
AGATAACAGAGCAAGACTCTGTCTCAAAAAACAACAACAACAACAACAATTCCTAT		
3970	3990	4010
GACTGAAAGTGACTAAAAAGCTGGCTTTATGCCATTAACACTCTGTACTTTGCAGCCAAT		
4030	4050	4070
CAGAACTGACGCAGTCTGGGTGCTAGCTGCTTCAAAAGCAACCCACACCACACTTTTACC		
4090	4110	4130
ATTTCCATACATCAACTGCTGAGAATATGAAAATGCACAGTGACAGGTTTTAGGATCCTG		
4150	4170	4190
CTTCAGGATTTTCCTTTTCCTGGTTTGGTCACTAGAGTTGGCTATTTATCTGTTTCTAAAC		
4210	4230	4250
AATAGCTATTTTATCGAATAGTTTAGAGACCACTATTAAATATTGTGACTGATGAAGGAT		
4270	4290	4310
CTGTGAATTTTTTTATATATGTTCTAAGAGTTACCATTTTGATACCTTTTAAAAACCAGC		
4330	4350	4370
AGCTTTCTACTATATTCATGTAAACAGCATGAATAAAACCATTTTTTGATACAGGGTTT		
4390	4410	4430

FIG. 7G

TATTTGGCTTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTTGATTTTACT

4450

4470

4490

ACCTTTTCAAAGATATTTTAAAAAGTGGATTACTACATATGATTTCTTTGGAGCTTACAT

4510

4530

4550

TTCTTTACTTCACGAATTCTATGTCACTGTTACAAGTTTCCATTCTGATGGCTTCTGGGC

4570

4590

4610

CTTTGTACCTTTGTTTTTGGTGCCTTATTCCTAGTATGTTTCTATCACCTTAATGAGGCC

4630

4650

4670

GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTTTCCAT

4690

4710

4730

CACCTTCCCCACTGATGCTCTGGGCGAGAGAGTGATGTGTCACCTCAACTGTGTGTAATA

4750

4770

4790

TGTCAGACACGTCCTACAATAACAGGCGTCATATTTGTATTATTTTAGTTTACTGTAGA

4810

4830

4850

AAATAATGTCACCGCCAAAGGTGATGAGAGTCACGTTTTGTAGGATCTGTTTTCTTATAC

4870

4890

4910

TTAAAGACAGACTTCTGCTACGGTAATTGCCAGTATTCATGGCTTCCTTTCTGTGTCAGA

4930

4950

4970

AGAGAAGGGATCTGCTTTCTCTTGGCTGATTTACATAGCATTGGTAATAGACATGCATT

4990

5010

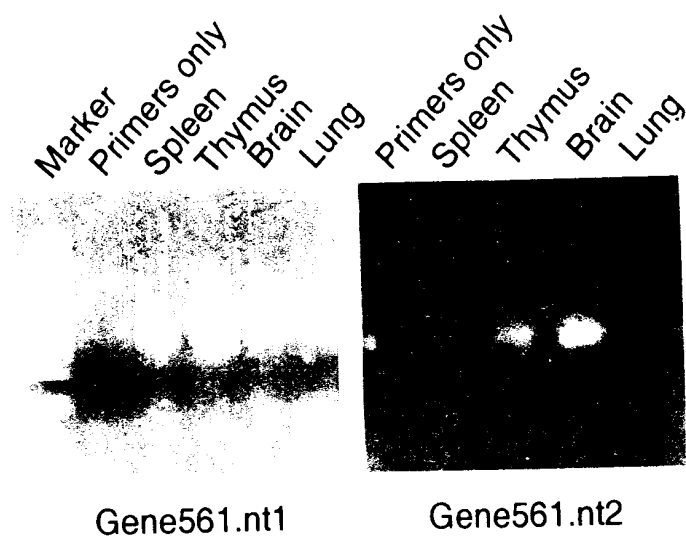
5030

TCTCTTTCTAAAGGGGAGTAACTTTTTAAACCCTTCCTGATTTTAGCCTGGCAATGTAAG

5050

5070

TGTCCTTAATGTGACTGTTTTGATAATTAAAAAAGGTATATAATTT



RT/PCR of Gene561.nt1 and Gene561.nt2

FIG. 8

10 30 50
 TCGAAACAGCTGCCGGCTGGTCCCGGCCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCCGG
 70 90 110
 GCTGTGGGGGCGCCGCGAGCTGGGCCGGCTCGGTGTGCCCGCGCCGCCAGCCCGCTCCA
 130 150 170
 GACGCGCCACCTGGGCGCTCCAAGAAGAGGCCGAAGTTGCCGCGGCCGTGAGTTGGAGC
 190 210 230
 TCGCGCCGGGCGCTGCGCCGGGAGCTCCGGGGGCTTCCCTCGCTTCCCGGTATTGTTTG
 250 270 290
 CAAACTTTGCTGCTCTCCGCCGCGGCCCCCAACTCGGCGGACGCCGGGCGCGGAGAGCCG
 310 330 350
 AGCCGGGGGCGCTGTGCGCAGCGCTCGGGCCAGGCCGGGCGGGCATGGGCGGGGGCCCCGA
 370 390 410
 GCAGGGGTGGAGAGCCGGGGCCAGCAGCAGCCCGTGCCCGGGAGCGGCGGCGCTGAGGGG
 430 450 470
 CGCGGAGCTCCCCGCGAGGACACGTCCAACGCCAGCATGCAGCGCCCGGGCCCCCGCCTG
 MetGlnArgProGlyProArgLeu
 490 510 530
 TGGCTGGTCCCTGCAGGTGATGGGCTCGTGCGCCGCCATCAGCTCCATGGACATGGAGCGC
 TrpLeuValLeuGlnValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg
 550 570 590
 CCGGGCGACGGCAAATGCCAGCCCATCGAGATCCCGATGTGCAAGGACATCGGCTACAAC
 ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn
 610 630 650

FIG. 9A

ATGACTCGTATGCCCCAACCTGATGGGCCACGAGAACCGCGGAGGCAGCCATCCAGTTG
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

670

690

710

CACGAGTTGCGCCCGCTGGTGGAGTACGGCTGCCACGGCCACCTCCGCTTCTTCCTGTGC
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

730

750

770

TCGCTGTACGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCGCCTGCCGGGTG
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

790

810

830

ATGTGCGAGCAGGCCCGGCTCAAGTGCTCCCCGATTATGGAGCAGTTCAACTTCAAGTGG
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

850

870

890

CCCGACTCCCTGGACTGCCGGAACCTCCCCAACAAGAACGACCCCAACTACCTGTGCATG
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

910

930

950

GAGGCGCCCCAACACGGCTCGGACGAGCCCACCCGGGGCTCGGGCCTGTTCCCGCCGCTG
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

970

990

1010

TTCCGGCCGCAGCGGCCCCACAGCGCGCAGGAGCACCCGCTGAAGGACGGGGGCCCGGG
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

1030

1050

1070

CGCGGCGGCTGCGACAACCCGGGCAAGTTCCACCACGTGGAGAAGAGCGCGTGTGCGCG
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

1090

1110

1130

CCGCTCTGCACGCCCCGGCGTGGACGTGTACTGGAGCCGCGAGGACAAGCGCTTCGCAGTG
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

1150

1170

1190

GTCTGGCTGGCCATCTGGGCGGTGCTGTGCTTCTTCTCCAGCGCCTTCACCGTGCTCACC
ValTrpLeuAlaIleTrpAlaValLeuCysPhePheSerSerAlaPheThrValLeuThr

1210

1230

1250

TTCCTCATCGACCCGGCCCGCTTCCGCTACCCCGAGCGCCCCATCATCTTCTCTCCATG
PheLeuIleAspProAlaArgPheArgTyrProGluArgProIleIlePheLeuSerMet

1270

1290

1310

TGCTACTGCGTCTACTCCGTGGGCTACCTCATCCGCCTCTTCGCCGGCGCCGAGAGCATC
CysTyrCysValTyrSerValGlyTyrLeuIleArgLeuPheAlaGlyAlaGluSerIle

1330

1350

1370

GCCTGCGACCGGGACAGCGGCCAGCTCTATGTCATCCAGGAGGGACTGGAGAGCACCGGC
AlaCysAspArgAspSerGlyGlnLeuTyrValIleGlnGluGlyLeuGluSerThrGly

1390

1410

1430

TGCACGCTGGTCTTCCTGGTCCTCTACTACTTCGGCATGGCCAGCTCGCTGTGGTGGGTG
CysThrLeuValPheLeuValLeuTyrTyrPheGlyMetAlaSerSerLeuTrpTrpVal

1450

1470

1490

GTCCTCACGCTCACCTGGTTCCCTGGCCGCCGCAAGAAGTGGGGCCACGAGGCCATCGAA
ValLeuThrLeuThrTrpPheLeuAlaAlaGlyLysLysTrpGlyHisGluAlaIleGlu

1510

1530

1550

GCCAACAGCAGCTACTTCCACCTGGCAGCCTGGGCCATCCCGCGGTGAAGACCATCCTG
AlaAsnSerSerTyrPheHisLeuAlaAlaTrpAlaIleProAlaValLysThrIleLeu

1570

1590

1610

ATCCTGGTCATGCGCAGGGTGGCGGGGGACGAGCTCACCGGGGTCTGCTACGTGGGCAGC
IleLeuValMetArgArgValAlaGlyAspGluLeuThrGlyValCysTyrValGlySer

1630

1650

1670

ATGGACGTCAACGCGCTACCGGCTTCGTGCTCATTCCTGGCCTGCTACCTGGTCATC
MetAspValAsnAlaLeuThrGlyPheValLeuIleProLeuAlaCysTyrLeuValIle

1690

1710

1730

GGCACGTCCTTCATCCTCTCGGGCTTCGTGGCCCTGTTCCACATCCGGAGGGTGATGAAG
GlyThrSerPheIleLeuSerGlyPheValAlaLeuPheHisIleArgArgValMetLys

1750

1770

1790

ACGGGCGGCGAGAACACGGACAAGCTGGAGAAGCTCATGGTGCGTATCGGGCTCTTCTCT
ThrGlyGlyGluAsnThrAspLysLeuGluLysLeuMetValArgIleGlyLeuPheSer

1810

1830

1850

GTGCTGTACACCGTGCCGGCCACCTGTGTGATCGCCTGCTACTTTTACGAACGCCTCAAC
ValLeuTyrThrValProAlaThrCysValIleAlaCysTyrPheTyrGluArgLeuAsn

1870

1890

1910

ATGGATTACTGGAAGATCCTGGCGGCGCAGCACAAAGTGCAAAATGAACAACCAGACTAAA
MetAspTyrTrpLysIleLeuAlaAlaGlnHisLysCysLysMetAsnAsnGlnThrLys

1930

1950

1970

ACGCTGGACTGCCTGATGGCCGCCTCCATCCCCCGCTGGAGATCTTCATGGTGAAGATC
ThrLeuAspCysLeuMetAlaAlaSerIleProAlaValGluIlePheMetValLysIle

1990

2010

2030

TTTATGCTGCTGGTGGTGGGGATCACCAGCGGGATGTGGATTTGGACCTCCAAGACTCTG
PheMetLeuLeuValValGlyIleThrSerGlyMetTrpIleTrpThrSerLysThrLeu

2050

2070

2090

CAGTCCTGGCAGCAGGTGTGCAGCCGTAGGTAAAGAAGAAGAGCCGGAGAAAACCGGCC
GlnSerTrpGlnGlnValCysSerArgArgLeuLysLysLysSerArgArgLysProAla

2110

2130

2150

AGCGTGATCACCAGCGGTGGGATTTACAAAAAGCCCAGCATCCCCAGAAAACTCACCAC
SerValIleThrSerGlyGlyIleTyrLysLysAlaGlnHisProGlnLysThrHisHis

2170

2190

2210

GGGAAATATGAGATCCCTGCCAGTCGCCCACCTGCGTGTGAACAGGGCTGGAGGGAAGG
GlyLysTyrGluIleProAlaGlnSerProThrCysValEnd

2230

2250

2270

FIG. 9D

GCACAGGGGCGCCCGAGCTAAGATGTGGTGCTTTTCTTGGTTGTGTTTTCTTTCTTCT

2290

2310

2330

TCTTCTTTTTTTTTTTTTTATAAAAGCAAAAGAGAAATACATAAAAAGTGTACCCTG

2350

2370

2390

AAATTCAGGATGCTGTGATACACTGAAAGGAAAAATGTACTTAAAGGGTTTGTGTTTGT

2410

2430

2450

TTGGTTTTCCAGCGAAGGGAAGCTCCTCCAGTGAAGTAGCCTCTTGTGTAACATAATTTGT

2470

2490

2510

GGTAAAGTAGTTGATTCAGCCCTCAGAAGAAAACCTTTGTTTAGAGCCCTCCSTAAATAT

2530

2550

2570

ACATCTGTGTATTTGAGTTGGCTTTGCTACCCATTTACAAATAAGAGGACAGATAACTGC

2590

2610

2630

TTTGCAAATTCAGAGCCTCCCCTGGGTTAAACAAATGAGCCATCCCCAGGGCCCACCCCC

2650

2670

2690

AGGAAGGCCACAGTGCTGGGCGGCATCCCTGCAGAGGAAAGACAGGACCCGGGGCCCCGCC

2710

2730

2750

TCACACCCAGTGGATTTGGAGTTGCTTAAATAGACTCCGGCCTTCACCAATAGTCTCT

2770

2790

2810

CTGCAAGACAGAAACCTCCATCAAACCTCACATTTGTGAACTCAAACGATGTGCAATACA

2830

2850

2870

TTTTTTCTCTTTCCTTGAAAATAAAAAGAGAAACAAGTATTTTGCTATATATAAAGACA

2890

2910

2930

FIG. 9E

ACAAAAGAAATCTCCTAACAAAAGAACTAAGAGGCCAGCCCTCAGAAACCCTTCAGTGC

2950

2970

2990

TACATTTTGTGGCTTTTAAATGGAAACCAAGCCAATGTTATAGACGTTTGGACTGATTTG

3010

3030

3050

TGGAAAGGAGGGGGGAAGAGGGAGAAGGATCATTCAAAGTTACCCAAAGGGCTTATTGA

3070

3090

3110

CTCTTTCTATTGTTAAACAAATGATTTCCACAAACAGATCAGGAAGCACTAGGTTGGCAG

3130

3150

3170

AGACACTTTGTCTAGTGTATTCTCTTCACAGTGCCAGGAAAGAGTGGTTTCTGCGTGTGT

3190

3210

3230

ATATTTGTAATATATGATATTTTTCATGCTCCACTATTTTATTAAAAATAAAATATGTTT

3250

TTTAGTTTGCTGCT

FIG. 9F

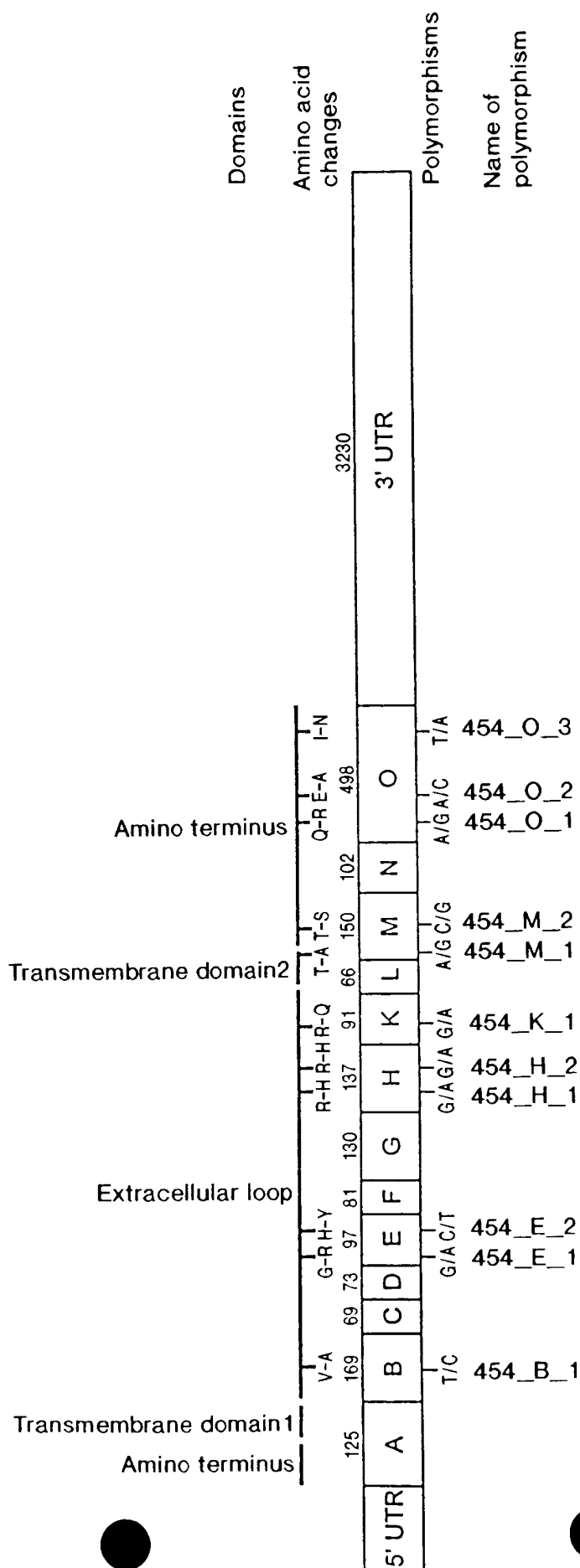
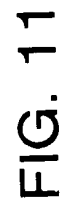


FIG. 10

Manhattan plot showing $-\log_{10}(p\text{-value})$ versus Location in kb for the 12p11.23 region. The plot displays various SNPs with their corresponding p-values and genomic locations. A horizontal dotted line indicates a significance threshold at $p=0.005$. The x-axis ranges from 0 to 14,000 kb, and the y-axis ranges from 0.0 to 2.5.

Key SNPs and their approximate $-\log_{10}(p\text{-value})$ values:

- ΔH_1 : ~2.4
- ΔE_2 : ~2.1
- ΔM_1 : ~2.0
- ΔF_2 : ~1.9
- ΔM_1 : ~1.8
- ΔO_6 : ~1.7
- ΔO_1 : ~1.6
- ΔL_1 : ~1.1
- Δ (unlabeled): ~1.0
- Δ (unlabeled): ~0.8
- Δ (unlabeled): ~0.7
- Δ (unlabeled): ~0.6
- Δ (unlabeled): ~0.5
- Δ (unlabeled): ~0.4
- Δ (unlabeled): ~0.3
- Δ (unlabeled): ~0.2
- Δ (unlabeled): ~0.1
- Δ (unlabeled): ~0.0



Chr. 12 Case(Asthma)/Control: Alleles

US

UK

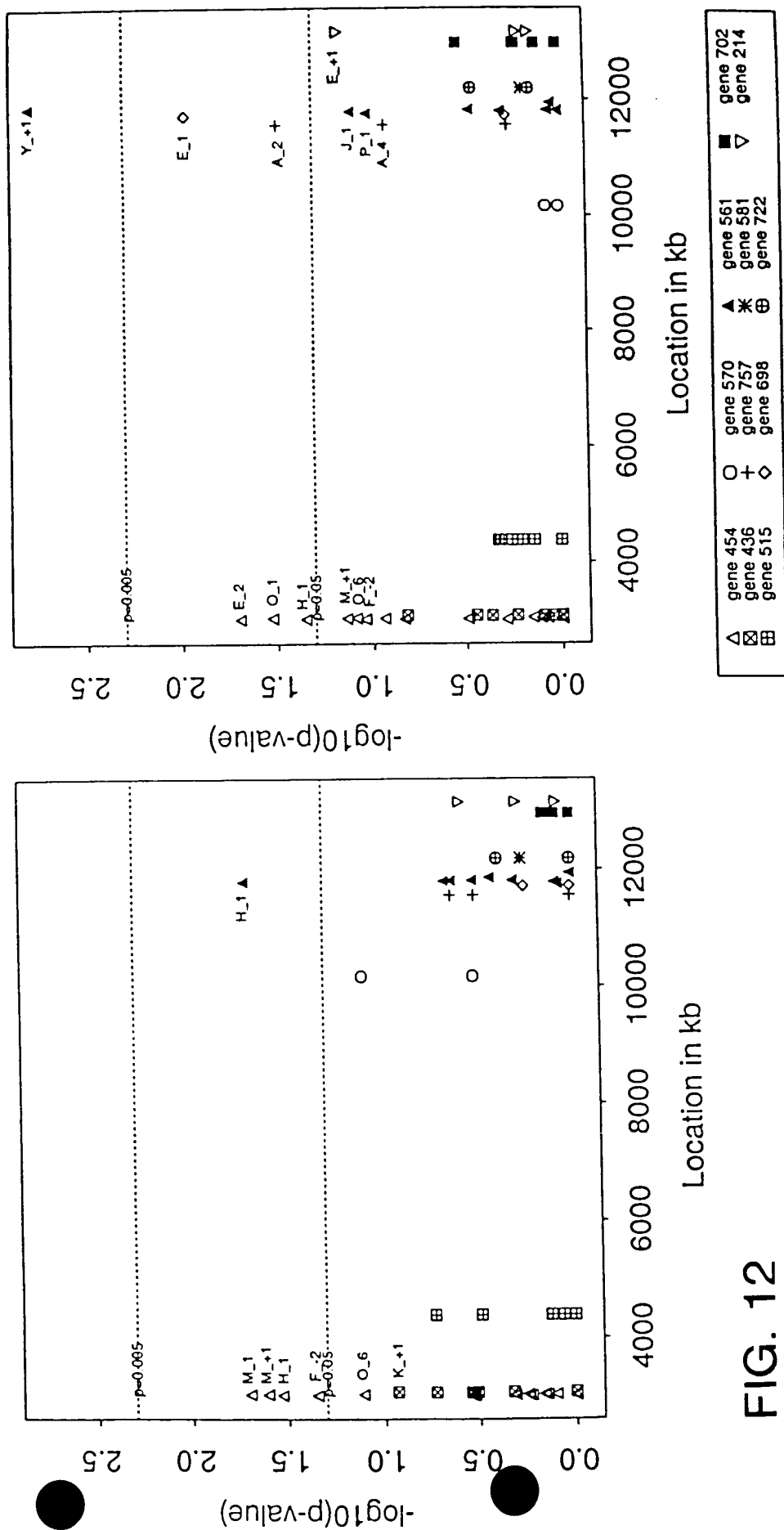


FIG. 12

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Alleles

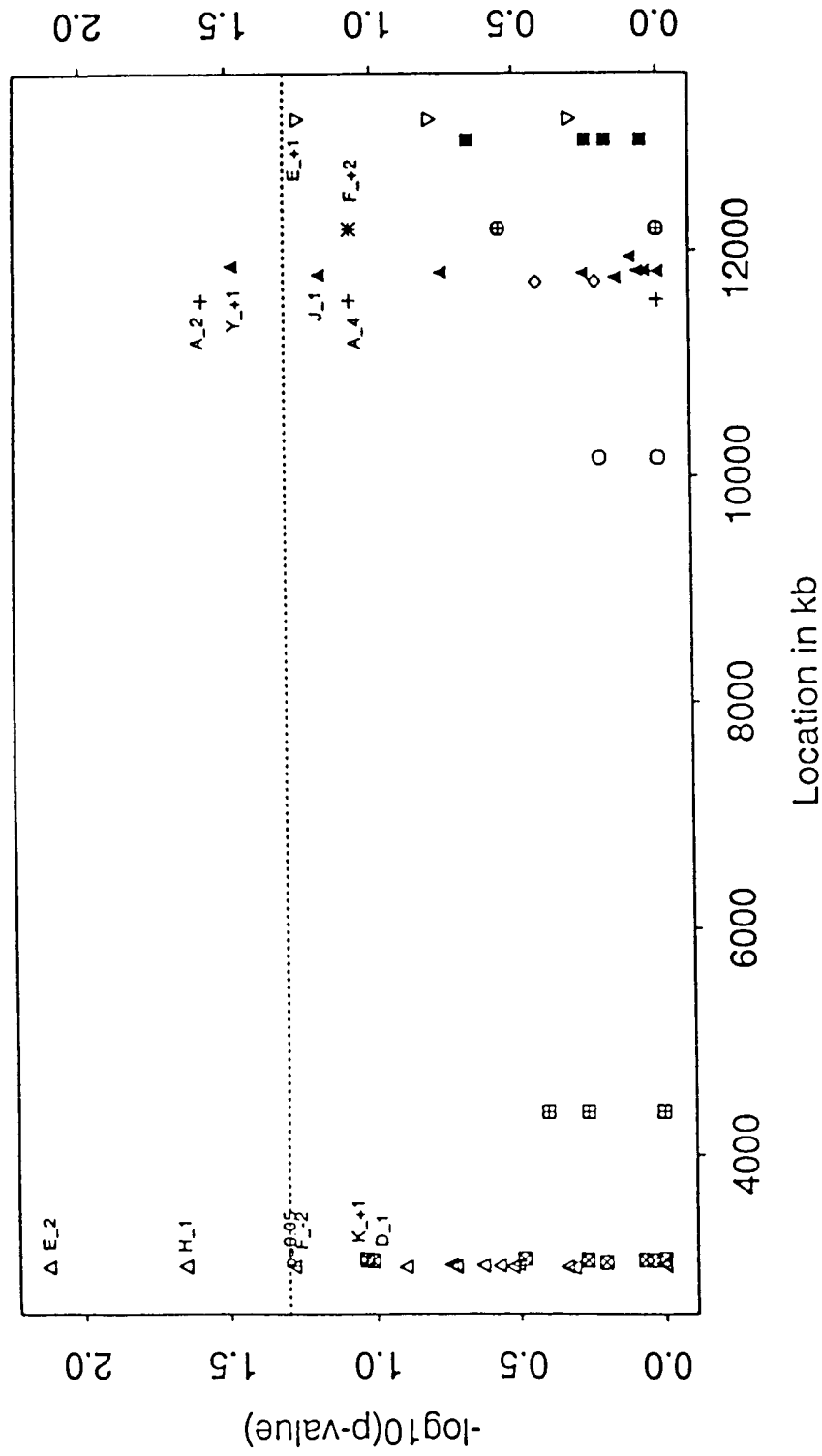


FIG. 13

UK



FIG. 14

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

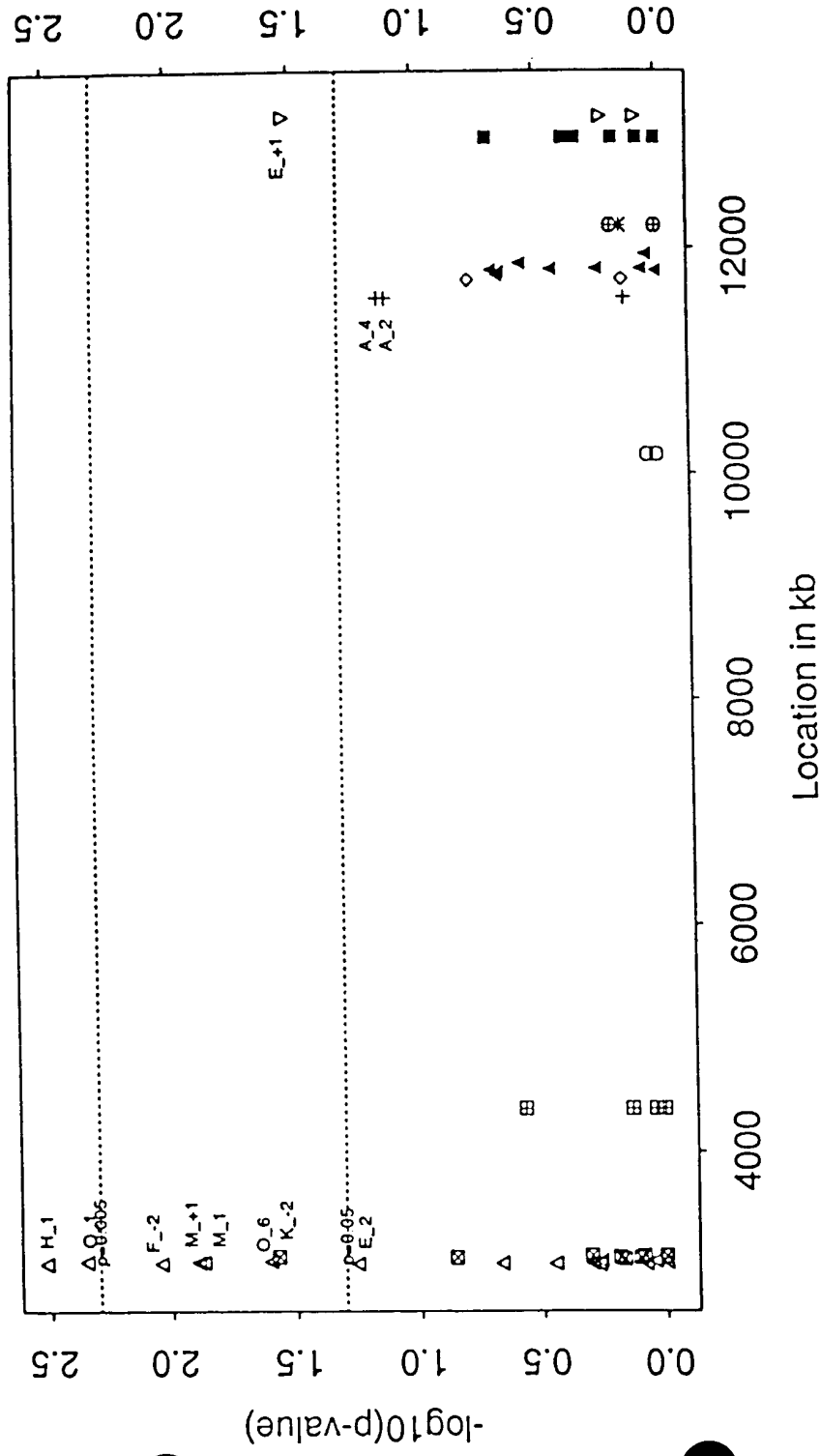
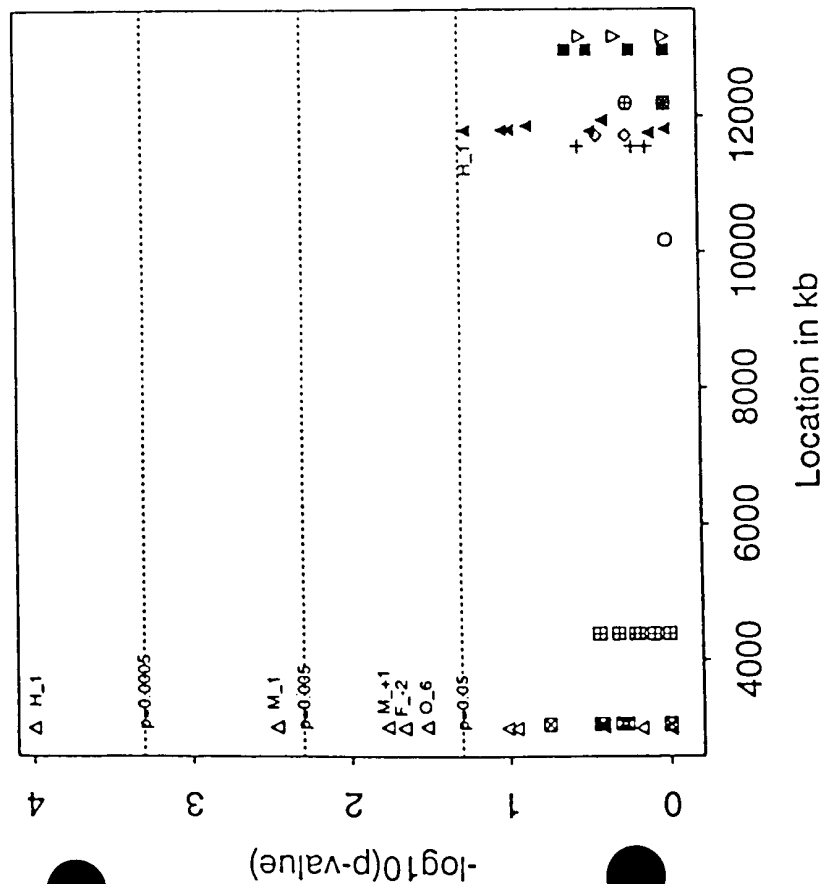


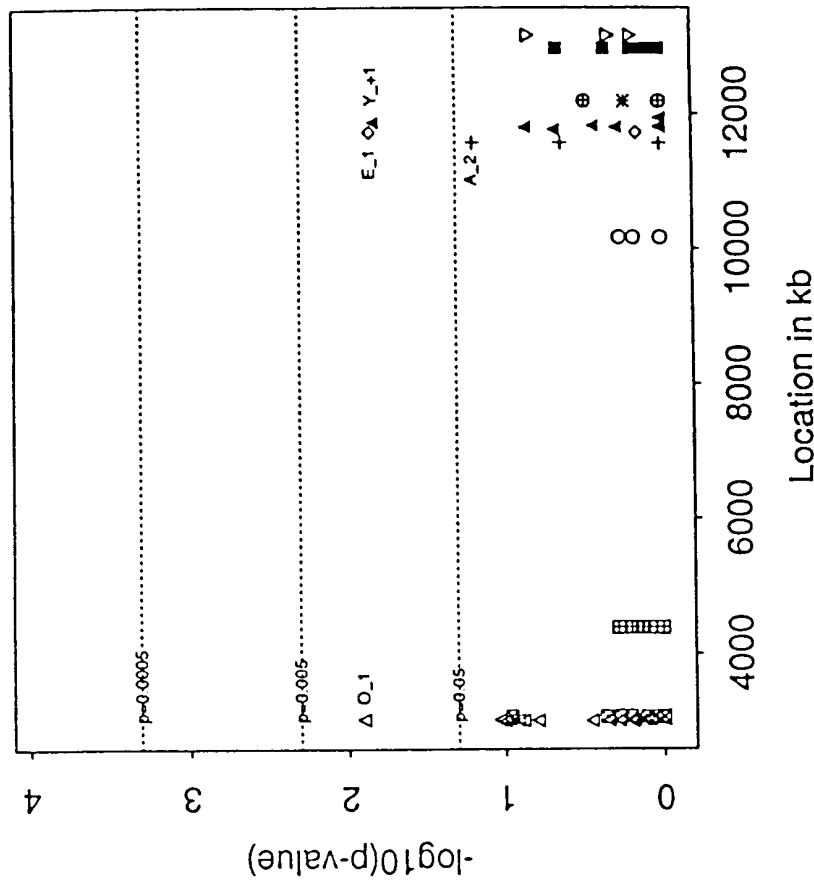
FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

US



UK



Δ	gene 454	\square	gene 561	∇	gene 702
\boxtimes	gene 436	$+$	gene 581	\star	gene 214
\boxplus	gene 515	\diamond	gene 698	\oplus	gene 722

FIG. 16

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

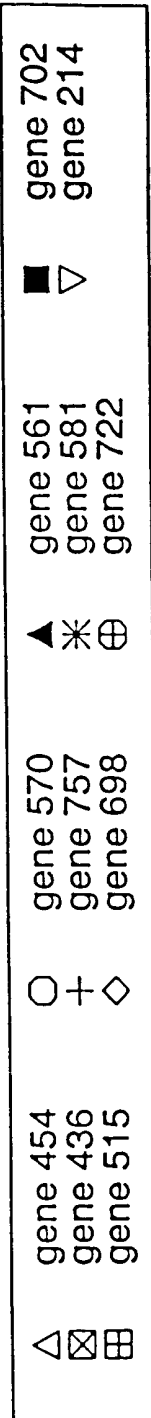
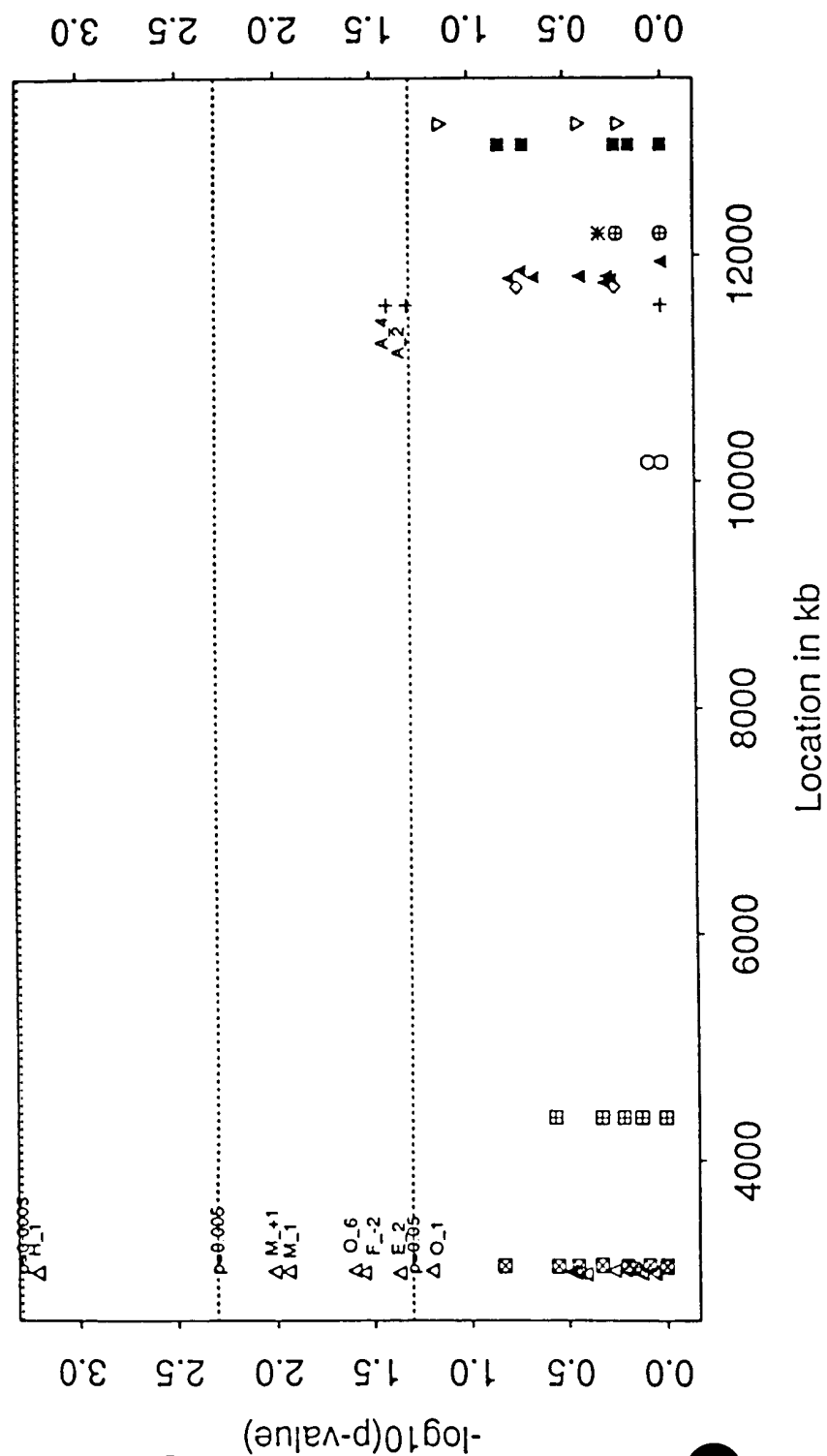
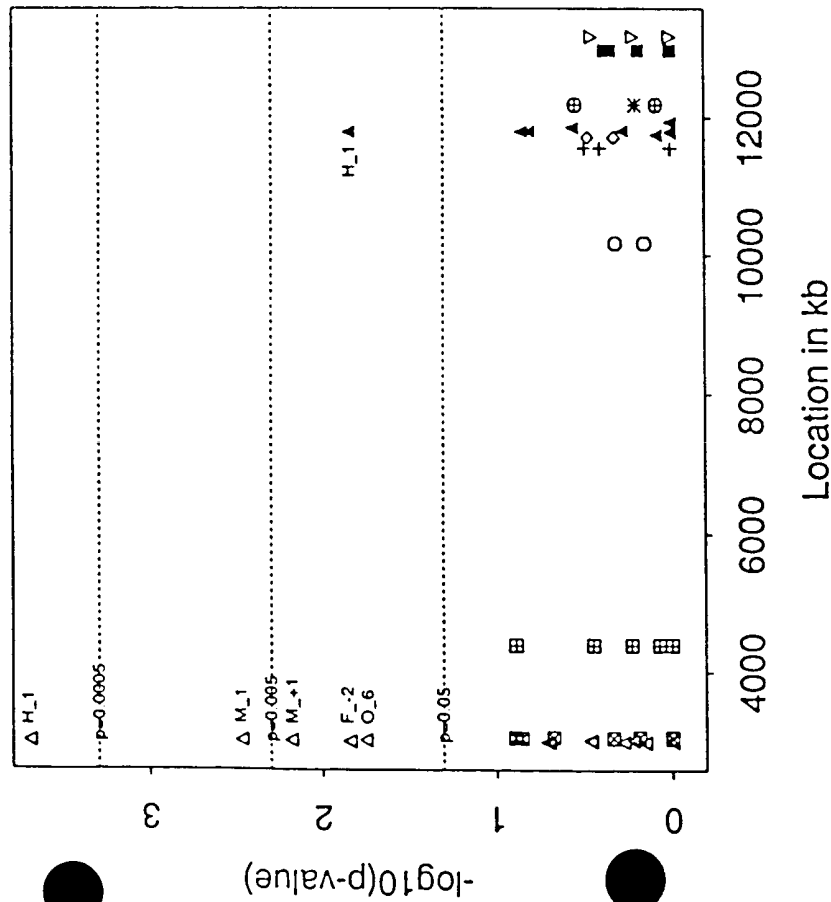


FIG. 17

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

US



UK

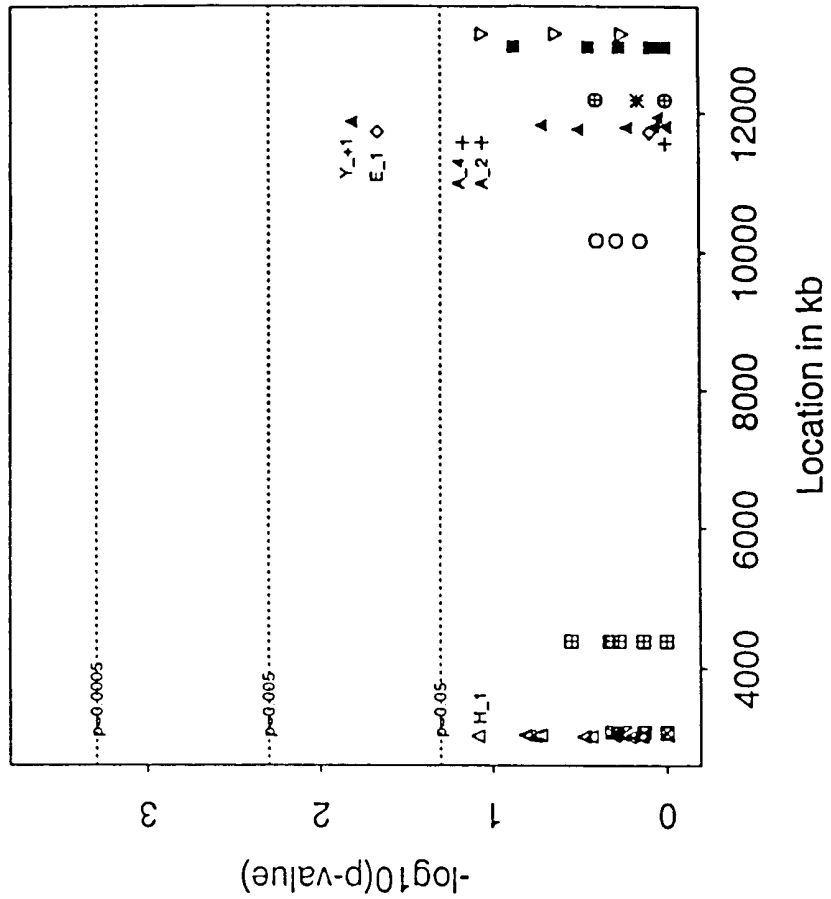


FIG. 18

Δ	gene 454	\circ	gene 570	\blacktriangle	gene 561	\blacksquare	gene 702
\boxtimes	gene 436	$+$	gene 757	$*$	gene 581	∇	gene 214
\boxplus	gene 515	\diamond	gene 698	\oplus	gene 722		

Chr. 12 Case(Asthma)/Control: Haplotype

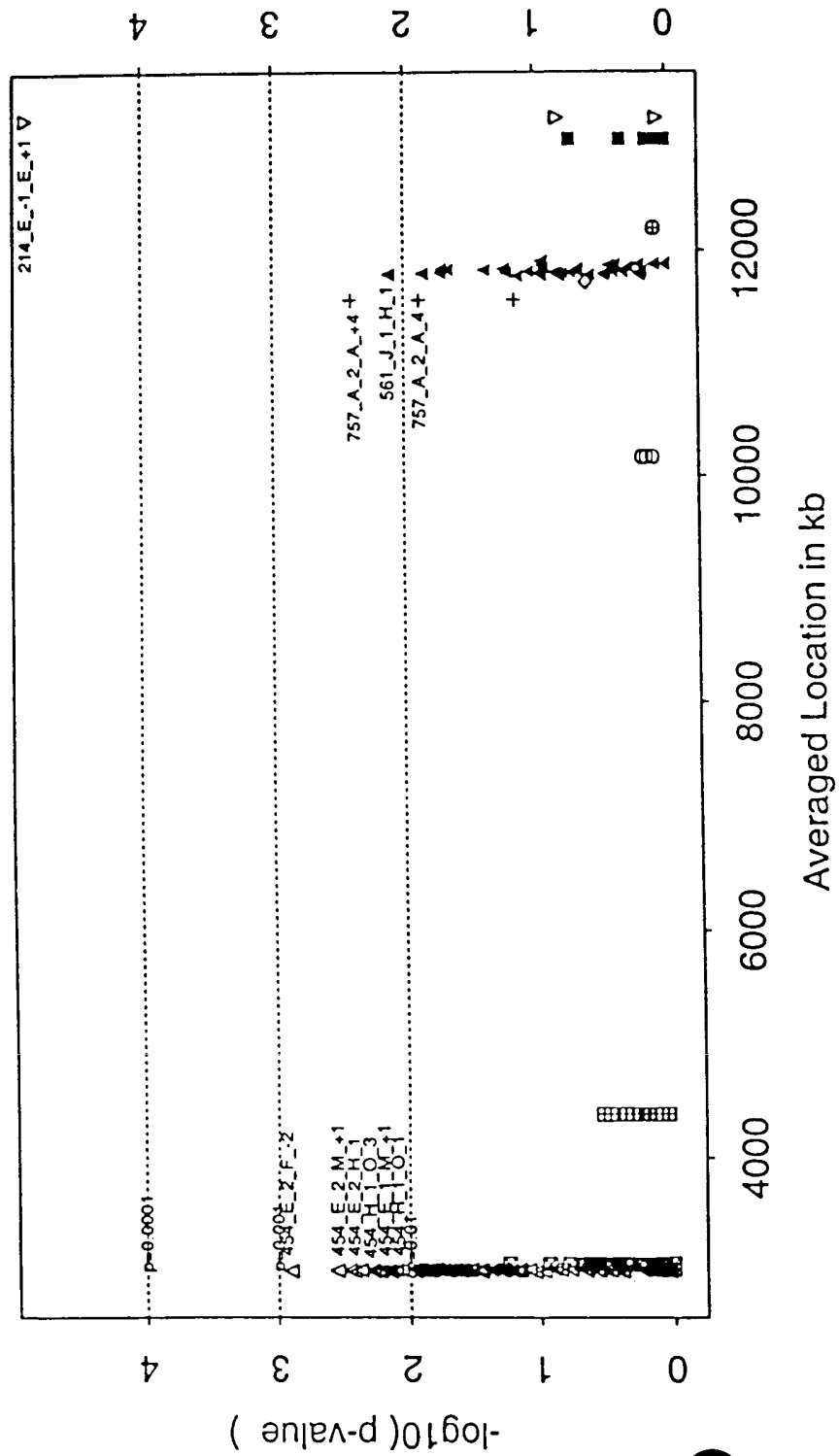
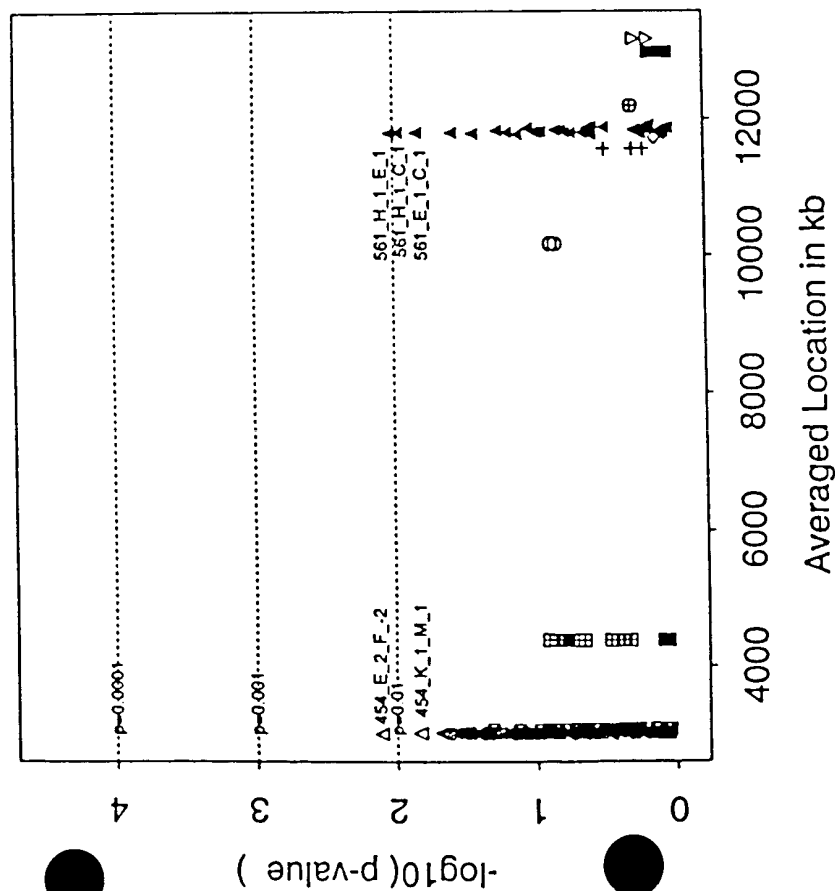


FIG. 19

Chr. 12 Case(Asthma)/Control: Haplotype

US



UK

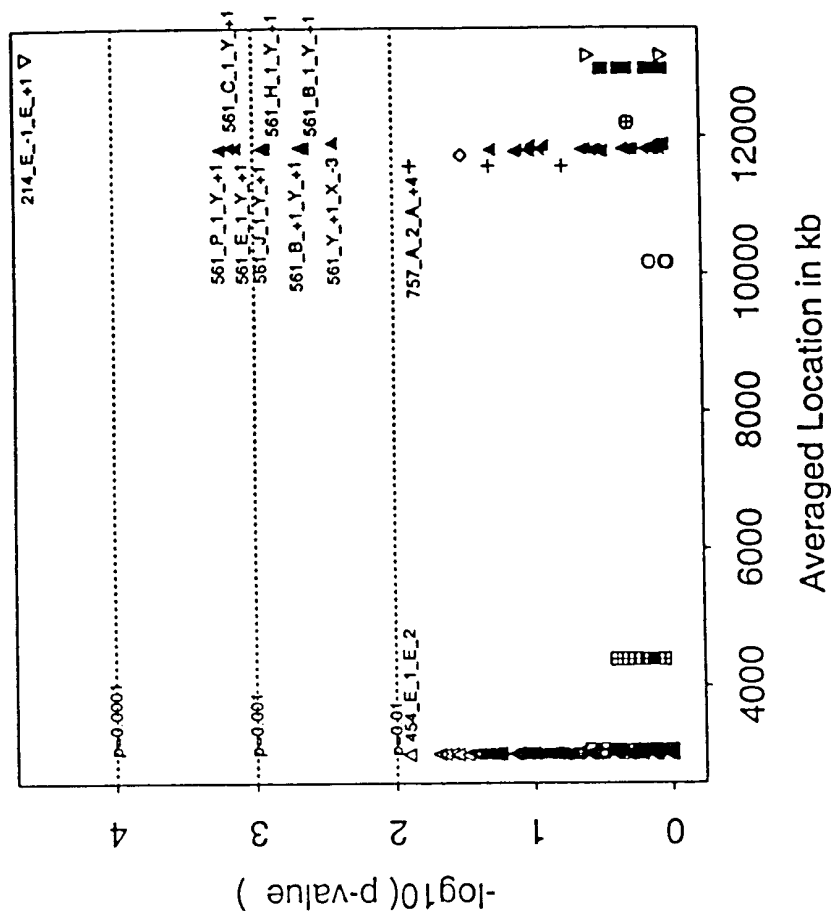


FIG. 20

Δ	gene 454	\square	gene 561	\blacksquare	gene 702
\boxtimes	gene 436	$+$	gene 570	\triangle	gene 722
\boxplus	gene 515	\diamond	gene 757	\oplus	gene 214
			gene 698	∇	

Chr. 12 Case(BHR (PC20 \leq 16 mg/ml) & Asthma)/Control: Haplotype

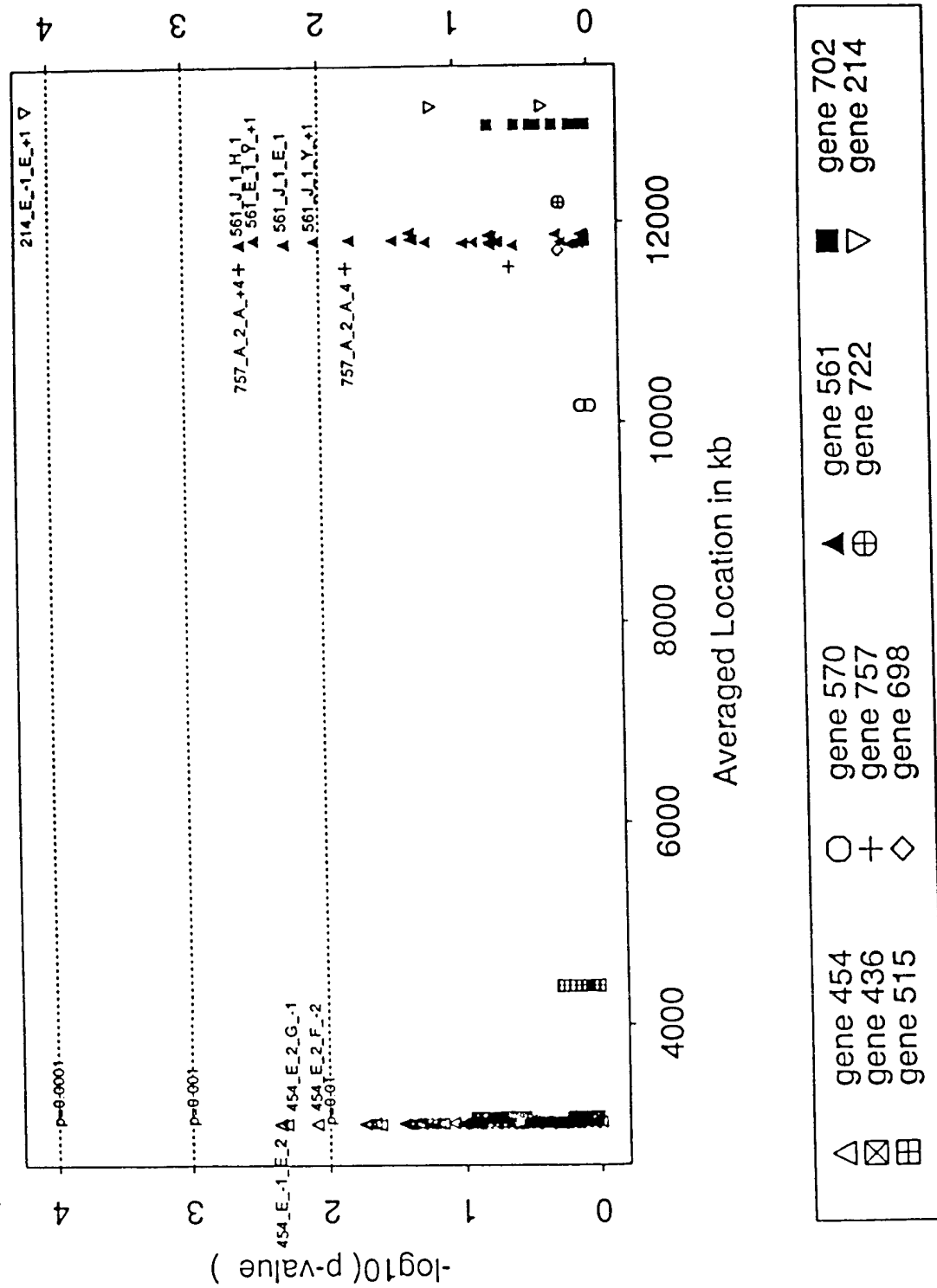
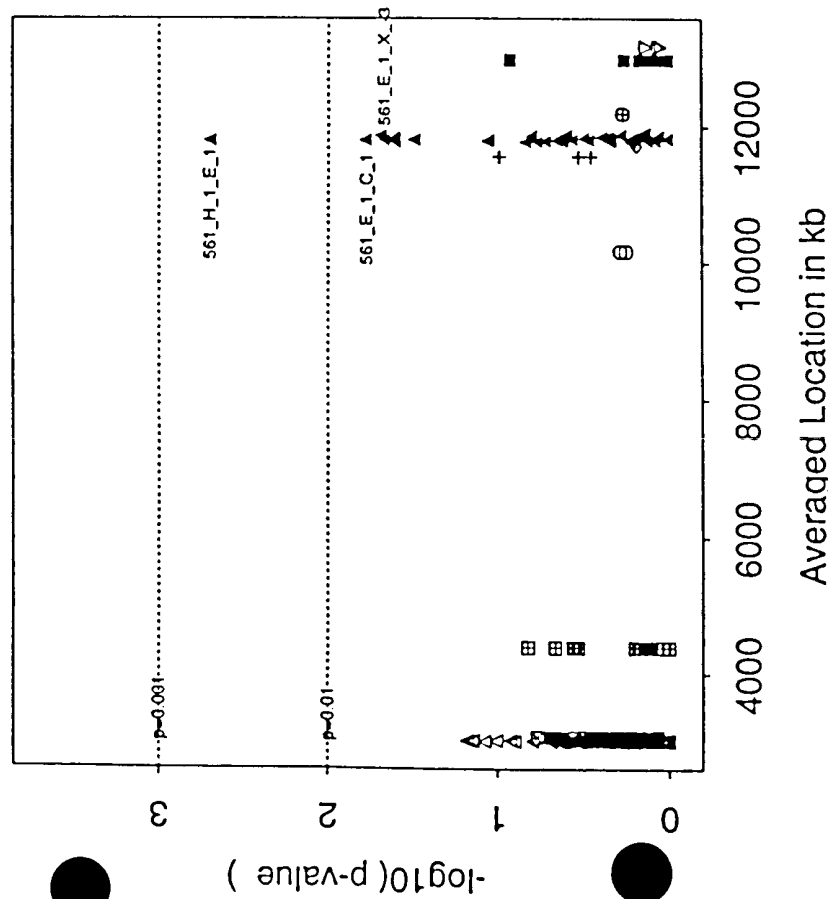


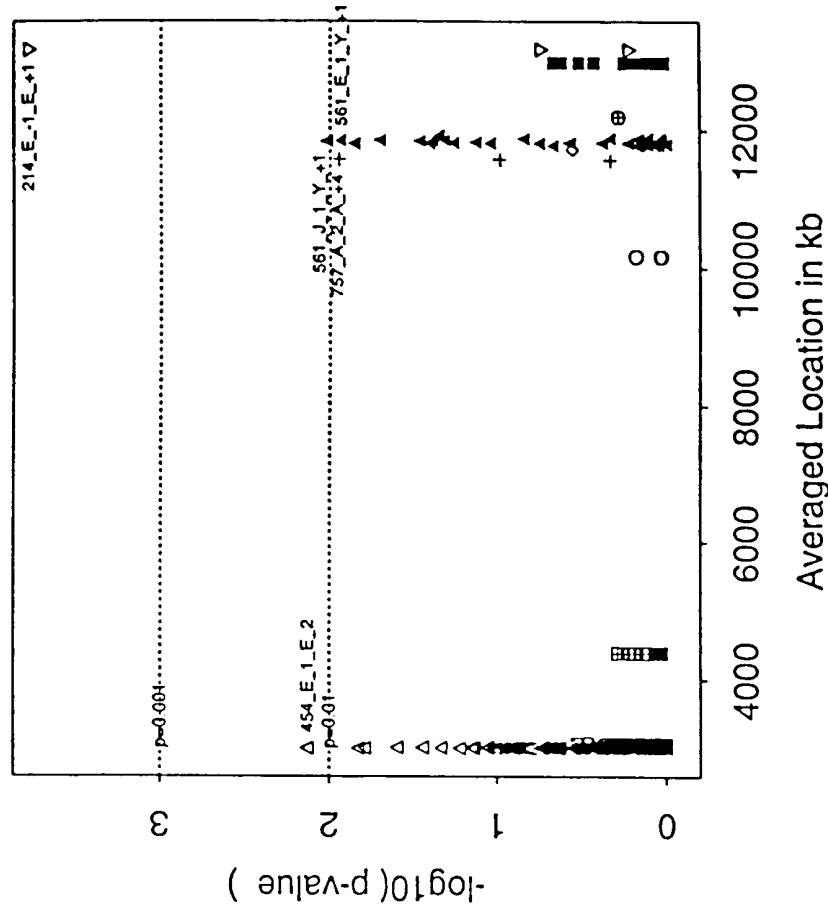
FIG. 21

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

US



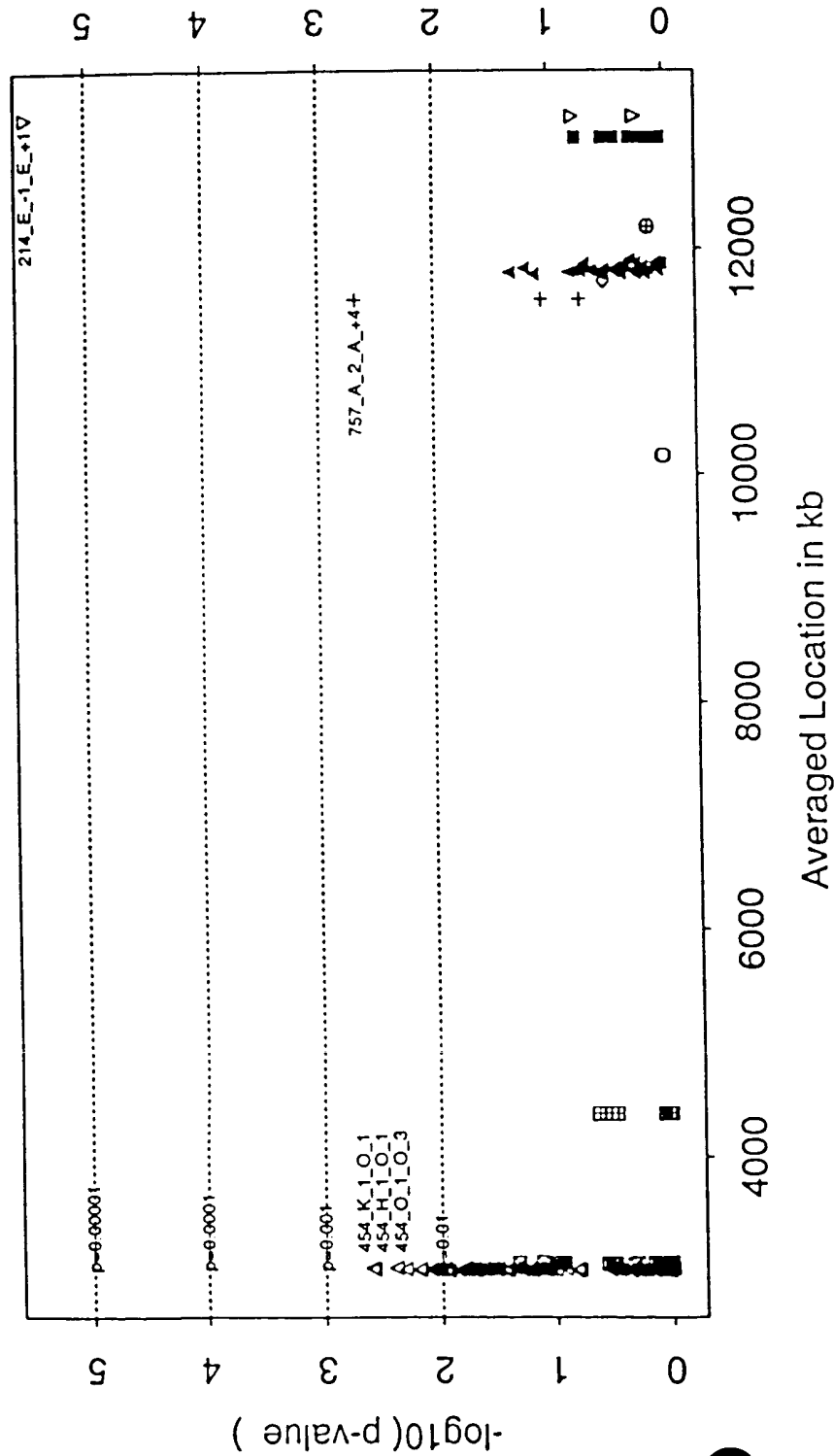
UK



△	gene 454	○	gene 570	▲	gene 561	■	gene 702
⊠	gene 436	+	gene 757	⊕	gene 722	▽	gene 214
⊞	gene 515	◇	gene 698				

FIG. 22

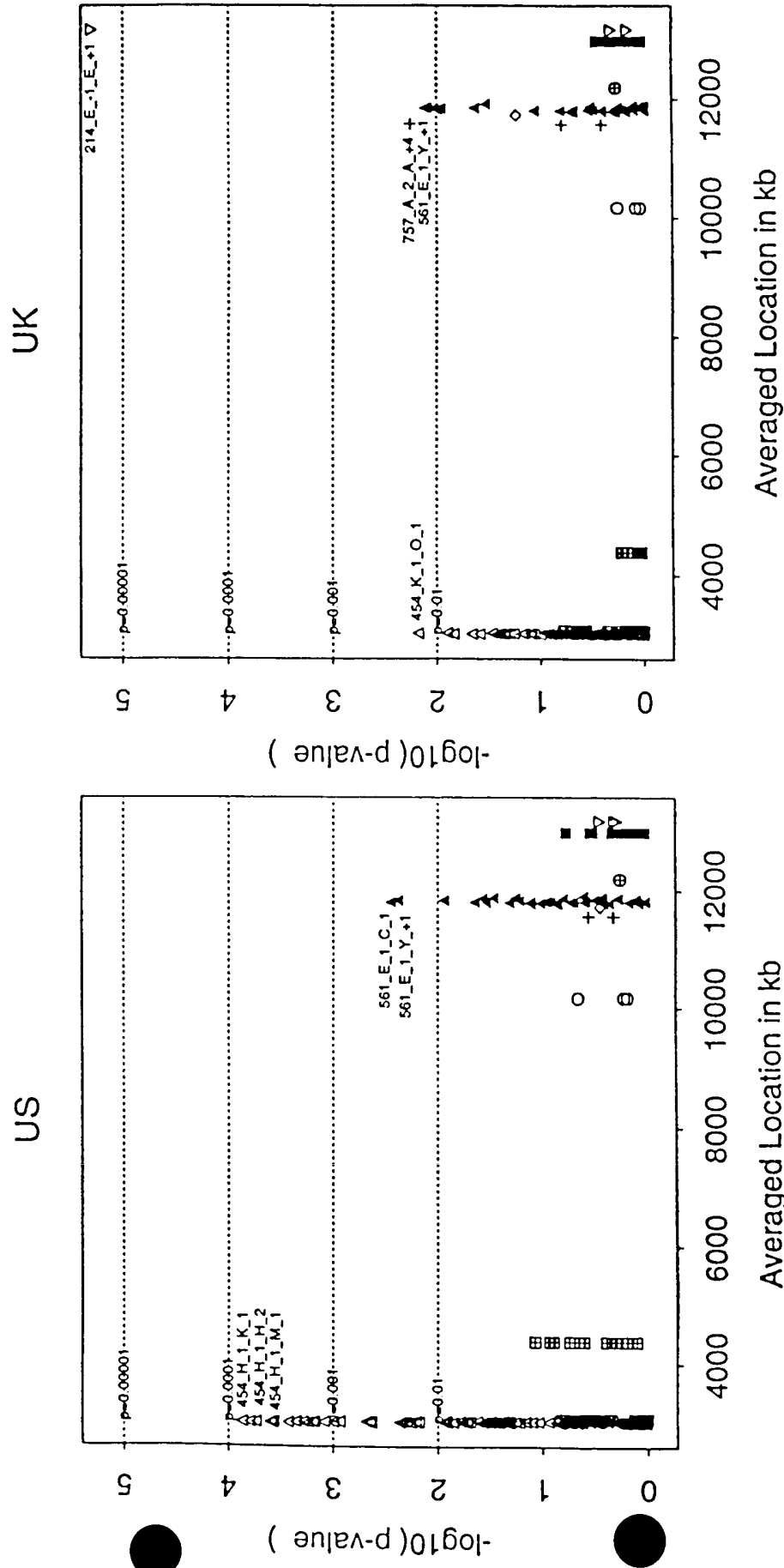
Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype



gene 454	gene 570	gene 561	gene 702
gene 436	gene 757	gene 722	gene 214
gene 515	gene 698		

FIG. 23

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype



△	gene 454	○	gene 570	▲	gene 561	■	gene 702
⊠	gene 436	+	gene 757	⊕	gene 722	▽	gene 214
⊞	gene 515	◇	gene 698				

FIG. 24

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

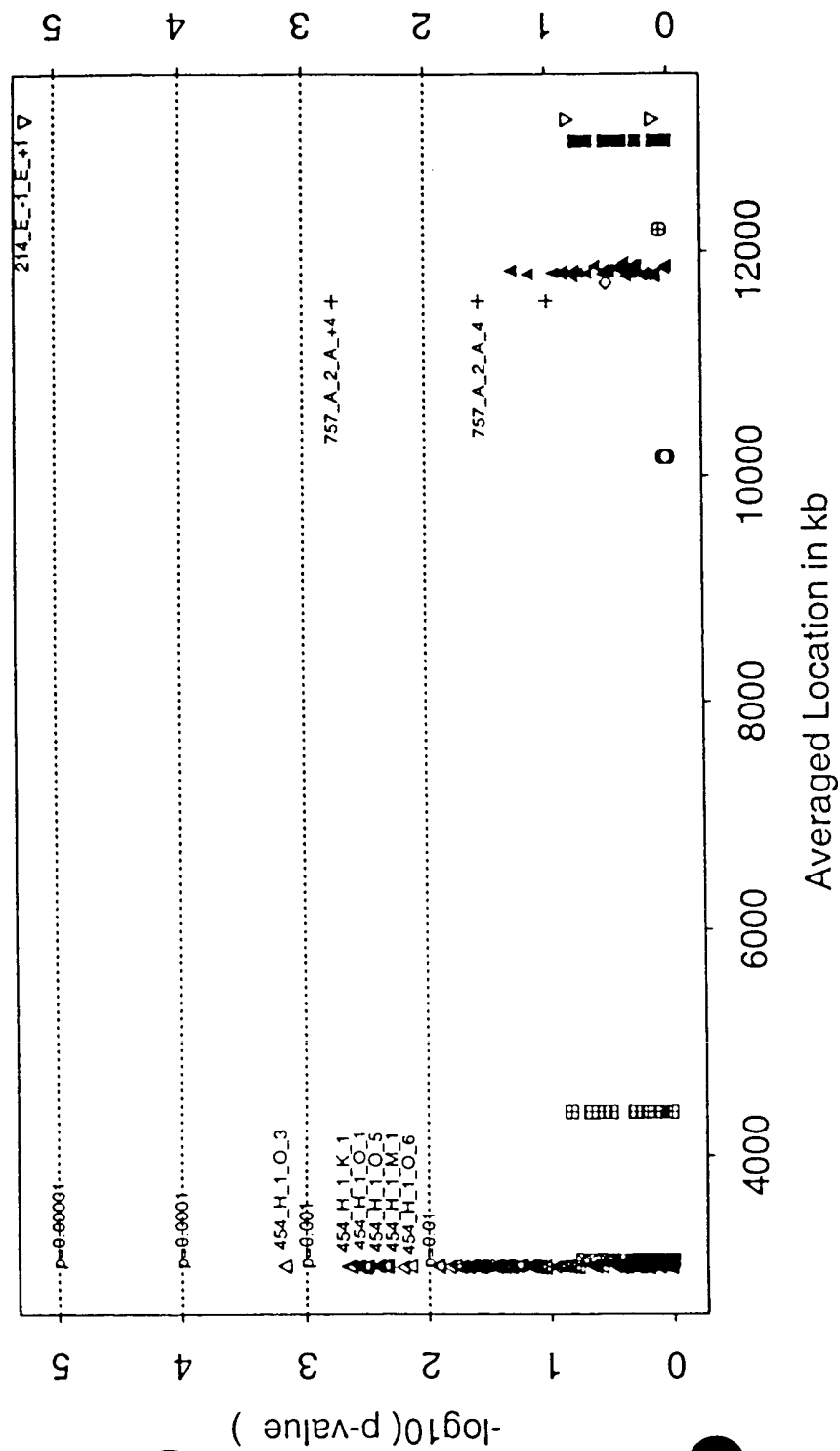
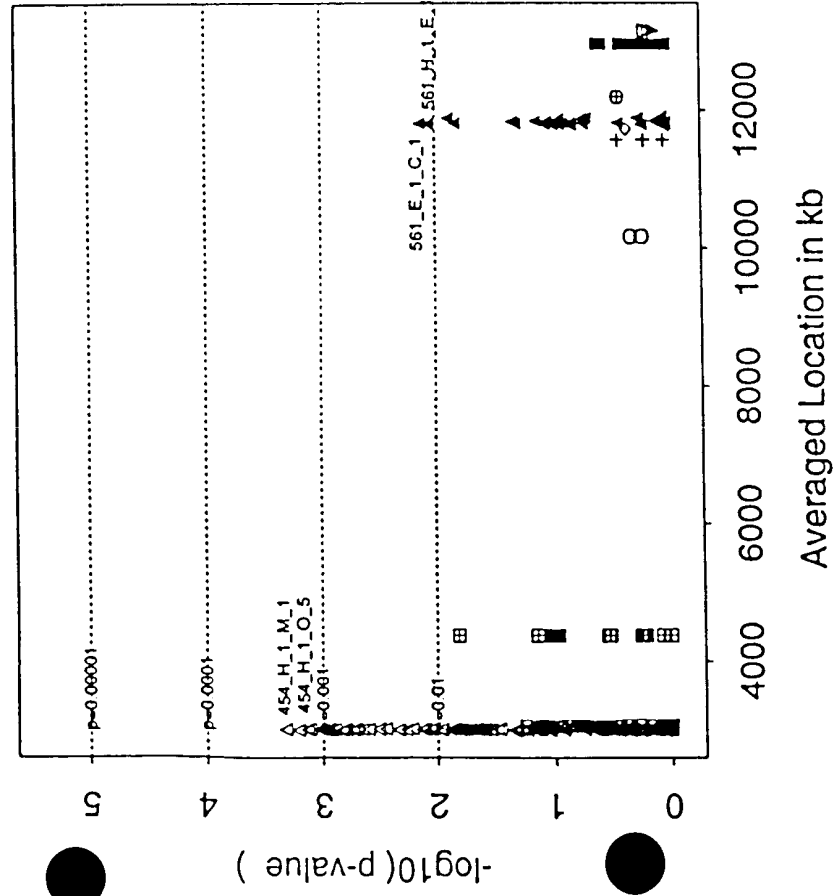


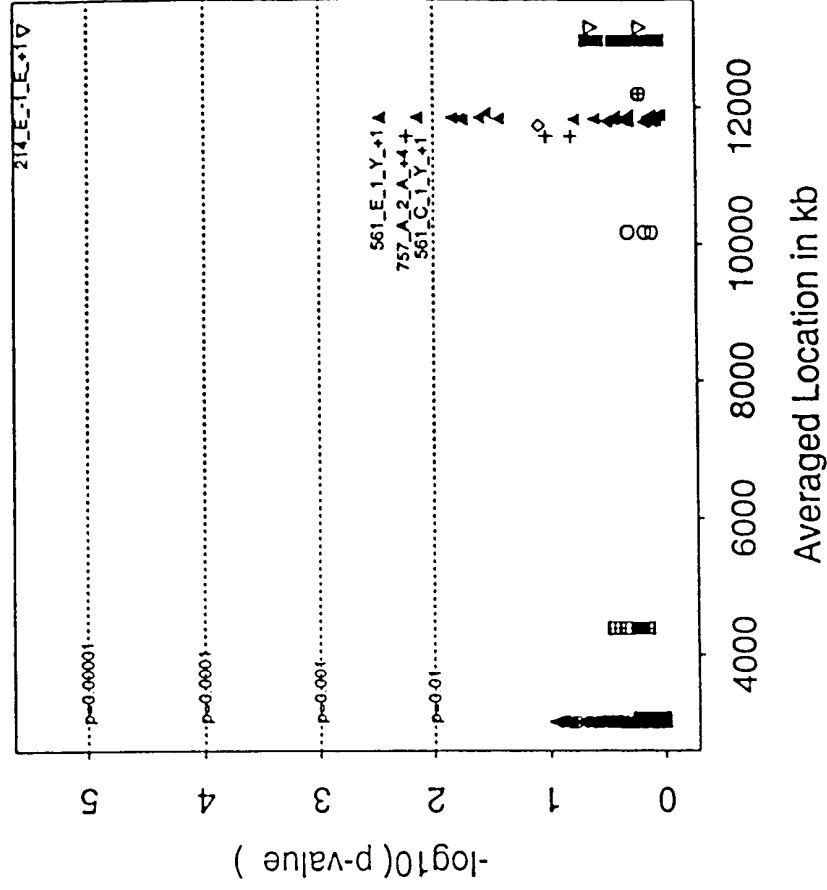
FIG. 25

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

US



UK



△	gene 454	○	gene 570	▲	gene 561	■	gene 702
⊠	gene 436	+	gene 757	⊕	gene 722	▽	gene 214
⊞	gene 515	◇	gene 698				

FIG. 26

10	30	50
CTTGAAATGACCCGCCACACCTGAAGCCTGCAGGTGCTGAGGCCACATTCGATCAGACC		
70	90	110
CAAGCTTTGGGAGACCGCTGGGGAAATTTCCCACTTCCTCTCCTGAGACCAGGAACCTCAG		
130	150	170
CAGAGAAACTTTGTGGAAAATGAACTGAAGGATGCCACCCAGGGAGAGTATCTCCTGAGA		
190	210	230
TCCCATCATGCAGGCCTTCCCACAAGGGCCCGGCAGCATGACAAGGTGAAGGCAGAGTAT		
250	270	290
GTGCATCTCAACCAYCCGCTCACCCCTCGTGACCAGAGAGCGCGATTGGCCGTGAAGGAG		
310	330	350
AAACACCAGCTCCAAGCCAAGCTGGAGAACCTAGAACAGGTCCTGAAGCATATGCGAGAG		
		MetArgGlu
370	390	410
GCGGCTGAACGGCGGCAGCAGCTGCAGTTGGAGCATGACCAGGCCCTGGCTGTTCTCAGT		
AlaAlaGluArgArgGlnGlnLeuGlnLeuGluHisAspGlnAlaLeuAlaValLeuSer		
430	450	470
GCCAAGCAGCAGGAAATTGACCTTCTGCAGAAGTCCAAGGTTCGAGAGCTGGAAGAGAAA		
AlaLysGlnGlnGluIleAspLeuLeuGlnLysSerLysValArgGluLeuGluGluLys		
490	510	530
TGCCGGACTCAAAGTGAGCAGTTCAACCTGCTGTCCCGGGACCTGGAGAAGTTCCGGCAG		
CysArgThrGlnSerGluGlnPheAsnLeuLeuSerArgAspLeuGluLysPheArgGln		
550	570	590
CACGCTGGCAAGATTGACCTGCTGGGTGGCAGCGCGGTGGCCCCCTGGACATCTCCACG		
HisAlaGlyLysIleAspLeuLeuGlyGlySerAlaValAlaProLeuAspIleSerThr		

FIG. 27A

610	630	650
GCCCCAGCAAGCCTTTCCACAGTTCATGAATGGCCTAGCCACCTCCCTCGGCAAAGGT AlaProSerLysProPheProGlnPheMetAsnGlyLeuAlaThrSerLeuGlyLysGly		
670	690	710
CAGGAGAGCGCTATTGGAGGCAGCTCTGCGATCGGTGAATATATCCGGCCCCCTTCCGCAG GlnGluSerAlaIleGlyGlySerSerAlaIleGlyGluTyrIleArgProLeuProGln		
730	750	770
CCTGGTGACAGGCCGGAGCCTCTGTCCGCCAAGCCCACCTTCCTGTCGAGATCCGGTAGC ProGlyAspArgProGluProLeuSerAlaLysProThrPheLeuSerArgSerGlySer		
790	810	830
GCAAGATGCAGATCTGAGTCAGACATGGAGAATGAACGGAATCCAATACCTCCAAGCAG AlaArgCysArgSerGluSerAspMetGluAsnGluArgAsnSerAsnThrSerLysGln		
850	870	890
AGATACTCGGGGAAGGTCCACCTCTGTGTTGCCCGCTATAGTTACAACCCCTTCGATGGA ArgTyrSerGlyLysValHisLeuCysValAlaArgTyrSerTyrAsnProPheAspGly		
910	930	950
CCGAACGAGAACCCCGAAGCTGAGCTGCCCTCACGGCGGGGAAAATACCTCTACGTCTAT ProAsnGluAsnProGluAlaGluLeuProLeuThrAlaGlyLysTyrLeuTyrValTyr		
970	990	1010
GGAGACATGGATGAGGATGGGTTCTATGAAGGAGAGCTCCTCGATGGCCAGAGGGGTCTG GlyAspMetAspGluAspGlyPheTyrGluGlyGluLeuLeuAspGlyGlnArgGlyLeu		
1030	1050	1070
GTGCCCTCCAACTTCGTGGACTTTGTGCAGGACAACGAGTCGCGGTTGGCAAGCACGCTG ValProSerAsnPheValAspPheValGlnAspAsnGluSerArgLeuAlaSerThrLeu		
1090	1110	1130
GGGAACGAGCAGGATCAGAACTTCATCAACCATTCGGGCATCGGCCTGGAGGGAGAGCAC GlyAsnGluGlnAspGlnAsnPheIleAsnHisSerGlyIleGlyLeuGluGlyGluHis		
1150	1170	1190
ATCCTGGACCTCCACTCCCCAACCCACATAGATGCGGGCATCACCGACAACAGTGCCGGG		

FIG. 27B

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

1210

1230

1250

ACCCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCTAGAAAAATC
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

1270

1290

1310

ACCCTCATCAAACAACCTCGCCAAAAGTGTTATTGTGGGCTGGGAGCCCCGGCGGTGCCA
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

1330

1350

1370

CCAGGATGGGGAACGGTGAGCAGCTACAACGTCCTGGTGGACAAGGAGACACGCATGAAC
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

1390

1410

1430

CTCAGCTGGGGAGCAGAACTAAAGCCCTCATCGAGAAGCTCAACATGGCAGCCTGCACC
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

1450

1470

1490

TACCGCATCTCCGTGCAGTGCGTCACCAGCAGGGGCAGCTCGGATGAGCTGCAGTGCACG
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

1510

1530

1550

CTGCTGGTGGGCAAGGACGTGGTGGTGGCCCCCTCCACCTGCGGGTGGACAACATCACG
LeuLeuValGlyLysAspValValAlaProSerHisLeuArgValAspAsnIleThr

1570

1590

1610

CAGATCTCCGCCAGCTCTCCTGGCTACCCACCAACAGCAACTACAGCCACGTCTCTTC
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

1630

1650

1670

CTCAACGAGGAGGAGTTCGACATCGTCAAGGCCGCCAGGTACAAGTACCAGTTCTTCAAT
LeuAsnGluGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

1690

1710

1730

CTCAGGCCCCAACATGGCCTATAAGGTGAAGTTCTGGCCAAACCCACCATGCGGTGG
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp

1750	1770	1790
CAGCTCCCGCTGGAGCAAAGGGAGAAGAAGGAGGCCTTTGTGGAGTTCTCCACGTTGCCT GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro		
1810	1830	1850
GCAGGACCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGGTGACCCCCGCCACC AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr		
1870	1890	1910
ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCCCACCGGGCTGTCCAATGGCGCAAAC IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn		
1930	1950	1970
GTTACCGGCTACGGCGTGTATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTTCCCCACG ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr		
1990	2010	2030
GCAGACAGCACGGCCGTGGAGCTTGTGCGGCTGCGGAGCCTGGAGGCCAAGGGCGTGACC AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr		
2050	2070	2090
GTGCGGACCCTCTCCGCCCAGGGCGAGTCCGTGGACTCTGCAGTTGCTGCCGTCCCCC ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro		
2110	2130	2150
GAGCTCCTGGTGCCTCCTACCCCCACCCGAGACCTGCACCCCAATCAAAGCCATTAGCA GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla		
2170	2190	2210
AGTTCTGGAGTCCCCGAAACCAAAGACGAGCACCTGGGTCCCCACGCCAGGATGGATGAG SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu		
2230	2250	2270
GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGGCACATGCTGGAGCCGCCCGTG AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal		
2290	2310	2330
GGCCCCGAAGGCGGTCGCCCTCACCCAGCCGCATCCTGCCGCAGCCACAGGGCACCCCG		

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350

2370

2390

GTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCCGAGAGC
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410

2430

2450

AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470

2490

2510

TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530

2550

2570

GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGCCGCACTGTTGCCATGGAGACGAGTAC
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590

2610

2630

CACACAGAGAGCAGCCGGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGluGlu

2650

2670

2690

CTGTATTCTGAAATGCAGCTGGAAGATGGGGGAAGGAGCGGCCAGCGGCACGTCCCAC
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgArgProSerGlyThrSerHis

2710

2730

2750

AATGCCCTCAAGATTTTAGGGAACCCAGCCTCTGCAGGACGGGTGGATCACATGGGCCGG
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770

2790

2810

AGGTTTCCCCGTGGCAGCGCTGGTCCTCAGAGGTCCCGGCCCGTGACAGTCCCATCCATC
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830

2850

2870

GACGATTACGGGCGAGACCGCTTTCTCCAGACTTCTATGAAGAGTCAGAACTGACCCT
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

2890	2910	2930
GGTGCCGAAGAGCTCCCGGCCCGGATCTTTGTGGCTCTCTTTGACTACGACCCGCTCACC GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr		
2950	2970	2990
ATGTCCCCAAACCCAGATGCTGCAGAGGAGGAGCTTCCCTTTAAAGAAGGCCAGATCATC MetSerProAsnProAspAlaAlaGluGluGluLeuProPheLysGluGlyGlnIleIle		
3010	3030	3050
AAGGTTTATGGTGATAAAGACGCTGATGGATTCTACCGTGGGGAAACCTGTGCCCGGCTT LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu		
3070	3090	3110
GGCCTTATTCCTTGTAACATGGTCTCTGAGATACAAGCAGATGATGAGGAGATGATGGAT GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp		
3130	3150	3170
CAGCTTCTTAGACAGGGCTTTCTCCCTCTGAATACACCTGTGGAGAAAATAGAGAGAAGC GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer		
3190	3210	3230
AGGAGAAGTGGCAGGCGTCATTTCGGTATCGACGCGGAGAATGGTGGCCCTGTATGACTAC ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr		
3250	3270	3290
GACCCAGAGAAAGCTCGCCCAACGTCGATGTCGAGGCCGAACCTACATTTTGCACAGGA AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly		
3310	3330	3350
GATATTATTACAGTTTTTGGTGAAATTGATGAAGATGGATTTTATTATGGGGAGCTGAAC AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn		
3370	3390	3410
GGGCAGAAAGGCCTTGTGCCCTCAAACCTTCTTGAAGAAGTGCCTGATGACGTAGAAGTC GlyGlnLysGlyLeuValProSerAsnPheLeuGluGluValProAspAspValGluVal		
3430	3450	3470
TATCTTTCTGATGCTCCATCCCCTACTCTCAAGATACGCCAATGCGCTCAAAGGCCAAAA		

TyrLeuSerAspAlaProSerHisTyrSerGlnAspThrProMetArgSerLysAlaLys

3490 3510 3530
AGGAAGAAGAGTGTTCATTTCATACCTTAATCAGGCAATGTAGCCTTCACGTAAGTGAGC
ArgLysLysSerValHisPheIleProEnd

3550 3570 3590
AACTGAAGATACCGATAAAGATACCAACTTAAGCTACCTTAACCGGGCCAGTGTGGTAGA

3610 3630 3650
CTTAAGGCTTCATTGTGGGGTTAAAAAAGATACAAAGAAATATGTCTCAAAAA

3670 3690 3710
ACTATTGGACCTAAATAATTAGAATATTACTTGGTCTCAGTTGTAAAGCAACTGAATTTA

3730 3750 3770
TAGTGAAGCAAATCATCTTTAATAATCATTTCTACTATTTGCATTAAGAAATTTGAAA

3790 3810 3830
GGCCAACATTGGGAACATATTTCTTAACAAGCTAACTGTGTGTTTACATAGAGAGAGCTG

3850 3870 3890
CATATTGCATTGTTAGCCACTCTTGGAAGCAACCTAACAAACATGTTTACTATAG

3910 3930 3950
GAAGCTTTACTTTAGAACTTAACCCAAGGTCAAGCAGATGAGTAGTGAACACAGGTGAT

3970 3990 4010
CGAGTGTGGCTCTGAACACTCCAAACACTGGCTCGAGTGGCCAGAACGTGTTTTCCTTA

4030 4050 4070
AGTAACCCTGCCTCTACCTTACGAGAGAGCTATGCTCCTCCTCAAAGCACAAATCATCCTG

4090 4110 4130
TGACAGAAGTTGCTGCAACACGCGTTTGTGTGGTATACCAATGCAATACTAAGTTGAT

FIG. 27G

4150	4170	4190
GAAGCACGCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTTCAGGTGTACTTT		
4210	4230	4250
GGGATGCTTTACTAGGTGTTTTCCATTAGAATTAGACCTTGATTTTAAATCCAAGCAAGC		
4270	4290	4310
TTGAAGCCCCCTTGGCTTACAGCATTTCGCTGCTGAATACTAAACACTCACATGGCAAGAG		
4330	4350	4370
TTGCTCTGGAGAGGTAGGGCCAGAGGAATGCTGCTGCACTGCCAACTCAGGCACATGCTT		
4390	4410	4430
AGCTGTAAAGGGAAGCGAGGTGAAGTCGTCCTGCAGCGTATTAGAGTAAAGTCTACCCC		
4450	4470	4490
TCTGAAGCACTATTAAGCGCTTAACGTATATTTAAATACTACCATGTGCTATCTACTGAG		
4510	4530	4550
GAAGATTCAATGTTCAATTATTTGGAAATAATGCAAGCATCCACTAAGGGCCTTTAAGCTT		
4570	4590	4610
TCTTTGATTATAATTAAGGTTCAATTTAGTTTTTTTTTTTTCTTTCAACCAGTGTCAT		
4630	4650	4670
CTCCAATATTTCTATAGTATACCAACCACCCAGGAATGCACTTTAACAATATCAGGATT		
4690	4710	4730
TTATATAACCAAATAGTTTCAAATACAACAAAATTCCCTTTATGAACTTTTCGCTTTTAA		
4750	4770	4790
GACTACTGATGGGTACTCGGCCAACTTTACTATCAACCTAATTCAGATCATGTCTCCCC		

FIG. 27H

4810	4830	4850
TGCCCTTAGTCTTCATTTATGAAGTGAATTATTACCTGCCTTAGCTTTGCCAAAGCAACG		
4870	4890	4910
GCCACCCCGCACTCCCTCGAGACAGAGAAACGGAACCCACACATTTATGTCTGGGGCCTC		
4930	4950	4970
TCTCTGGCGTGCTGTGGGAGAGGACCTTTGCTTCTCATGGCATACTTCAACAAGTAAAG		
4990	5010	5030
AACAAATGAACCCCTGACCTTTCCTGGTGGGAAACGGGGACAGTACGATGTTACCAAG		
5050	5070	5090
TGAATTCTGTTGTTGGCGCTCACACACTCAATAAACTGTAACACTGTACCTACTAGGTTT		
5110	5130	5150
CTCCTGAGGGTTCAGGTACAGCAAGGAGAGCTCCATCCCCACAGTCCATCTCCATTCCG		
5170	5190	5210
GGTCACCTACGTCATCTATGGGTTCTGGTAGTCCTGGGAGAGGCAGGGAAATGTCTCTGA		
5230	5250	5270
AAAAGAAAAAGGGGCTGCTTTCCAAAGGCAAGAACTGCTGAAAAAGCTGGGTGCAGTGA		
5290	5310	5330
AATGATTATGTGCTTCCGGACAAGTCCAAATCTATGTAATTTCTTTAATCCAAACT		
5350	5370	5390
AGGGCTTTTATGACTCAAGTACTTCCTAAAAAACCCTTCTCTCCCTGACACCAAGT		
5410	5430	5450
GAGAAATGCACCTTTGCACTACCAACCACTTTAAACCAACCAAGAGAGGAGCG		
5470	5490	5510

GTTGCTCTCTGTCACCGCTGGCAGTCTGCTCTCATTGTCCAAGCTCTGATTGGGAGGTG

5530

5550

5570

GGAGGGGACGTCTTATTAACAAACGGGGGCGCATAGCTATCACCTGTAGTCCCTCCCTA

5590

5610

5630

CCTGTAATTCCAGTCTTTGTGCATTTGTCATCTGCCCTTAAAGGAATGATTTCAACCTT

5650

5670

5690

TCTCCCTTCTCAAATGCTTGCCTCATAATGCATAACTTTCACTTTGACTCTGGTCTTGA

5710

5730

5750

AATTCCTAGTTTAATTCGCCTTGATGTTCTGCCTTATAAATGCACAATGATTTGTACTGT

5770

5790

5810

CTAATAAAAACAGTGTATACTTTGTATGTGTCGTGCATTTCAGTGGTCTTCATCCTGACAC

5830

5850

5870

AGTGGTTCGAGATCAAGTTGTACAGGCTGTGCATTTTAAGATACTAGTTTCAGTCTTTCA

5890

5910

5930

AAGCCAGCCAGGCTACACACAGAAAATGTTTACTCAATCATTCAAAAAAGAGAAAAGGAG

5950

5970

5990

AGAAAGTAACTTTGTTTGGTAAAGCACCAGTACTCCAACCTTCCAGAAAGCCGATTATCT

6010

6030

6050

TCATTGCTTTTAATGTTCTATTCTGTGGCÄTATGGTTTTCTGTTACTTTCTGTTGTCAAAA

6070

6090

6110

TGCCATACCCAAATACACAGCAATGAATGGCACACAAGTAATCCACATAATGCATAAGCC

6130

6150

6170

ACACCAAAAACCAGACTCAATTTAAATCTGCTCCAAATGAGTCCATACCCATCTTCATCAT

6190 6210 6230
TGGCATTGAAACAAAAGACTTACTTACAAAGTTGCTGGCAGATGTATTTGATGGTTACTC

6250 6270 6290
TTTTGTAATTCTTGTCCTTGTAAATTGTTTTACTCTTTATACATACTTTTCAGACTG

6310 6330 6350
CCTTTCTTTTGTAAATTTATGGACGGTTTATAAATGAATGACAAAGCTTTCCCCATTGTGT

6370 6390 6410
CTTCAAAAACGCTATTATAAATTGTAATATAATAGTATGTGGTAGATTATTATTAAAGG

6430 6450 6470
AAATCCATGTGTGGTTAAGCTCTGTGTGGGTGTGTGCATGTGCACAGTTAGTGTAATAA

6490
TTTCTAGAAATAAAATTTGTTATTTTAT

FIG. 27K

10	30	50
GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAAGCCTGTGCACCTGGCCCTGTGC MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys		
70	90	110
ATGGGCACATGCTGGAGCCGCCCGTGGGCCCCGCATCCTGCCACAGCCACAGGGCACCCC MetGlyThrCysTrpSerArgProTrpAlaProHisProAlaThrAlaThrGlyHisPro		
130	150	170
GGTGTCCACCACCGTCGCCAAGGCCATGGCCCCGGGAGGCCGCGCAGAGGGTGGCGAGAGC GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer		
190	210	230
AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla		
250	270	290
TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp		
310	330	350
GACTTCCTGAAAGGCTCTGAACTTGCAAGCAGGGAAACTGAGGCCACAGAATTGAGAA AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd		
370	390	410
TTTTTGTCATGATTACGCAGATGGTCTCCTAACAGAGCTGGAATTAGATTGAACCGAGG		
430	450	470
CCTGAAGAAGACCTGTTCCACGCCTTTCCCCATGTGCCACGTTCTCCTCACCTATCCAG		
490	510	530
GAGTGAATCATCACCTTCCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA		
550	570	590
GCACTTGTTCTCTGGGTGAAGGACCCATACCCCCACTGGTTTTTTGAGATCGGCATTACAGC		

FIG. 28A

610	630	650
GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGCCCTTGACATGTGGCCACCTG		
670	690	710
GGGCTGAGTGTGACTGAGGCCCTGAATTTTTACTTCTATAAAATTAGTTCCAGATTAGTT		
730	750	770
TACATTCCTAATTAGTTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA		
790	810	830
CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTTCTAGAGAAGAGTAGAA		
850	870	890
ACACAGCGGCAGAAACACAGCTCTGCACTTCCGAGGGCCTCCCACTCCTTCTGATGAGAC		
910	930	950
TGCAGAGGAAGTCTGTTTGGCCAAGCATGCTATTAACACGTTTTCCTGCTTGTTTTGTTT		
970	990	1010
TTTAACAGAGCAAACAGGTCTGTTTCTATTAAAATTTAAAAGCGTTAATATTTARCAGC		
1030	1050	1070
ATTGTTTTATGTTGTATTCATAACATAATAATATAACAATATATTAATTGTTAATATATA		
1090	1110	1130
TTGTTAATAATATAATAATATAACATAAAATAAGTGATACTTATTTTCCATTTACAGTTG		
1150	1170	1190
AGATATTTTCTTTAAAAGTAACGTAAATATTGATTCAATTCAAAGAATACATTCATTAA		
1210	1230	1250
TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT		
1270	1290	1310

FIG. 28B

TGAGCTGGTGCACAGACTGCCAGTTTTACAACCCGGGAAGTGTTCCCTGACCATCCGCTT

1330

1350

1370

CCCCATGCTGCCCCGCCCGTCACATGAGCCCTTACCCCTGGCGCTATCCCATCTGCTCC

1390

1410

1430

AAGACACCGATGTTCTAGTGGGTGGAAGCCTCCACTTTTAGTTGACTACGGTATCTCTAG

1450

1470

1490

CATTTACACATAGTAGGTGCTCAATGAATGTTTGTGCAATGAATGAATGAAAGAAGGGA

1510

1530

1550

GGCTGAGAGTAGCTGGGACATTTGCTCTGAAAAATCACCTCCATTCTCCCAATATTACA

1570

1590

1610

AAAGCATTTTCATTAAGTCCACAATGAAAAATGCTCACTGTACCAATAAATAATATCTTT

1630

1650

AGTTATCTATTTTTAAAGTAAAAAAAACCTCGTGCCGAAGTC

FIG. 28C